IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s):	Pergolizzi et al.	
Serial No.:	08/479,995	Group Art Unit: 1631
Filed:	June 7, 1995	Primary Exam'r: John S. Brusca
For:	**ANALYTE DETECTION UTILIZING POLYNUCLEOTIDE SEQUENCES, COMPOSITION, PROCESS AND KIT** (As Previously Amended)	

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REQUEST FOR VOLUNTARY PUBLICATION OF PATENT APPLICATION
(UNDER 37 C.F.R. §1.221(a))

Dear Sirs:

This paper follows the May 14, 2010 Decision [Bd.R. 125(c) on request for rehearing] entered by the Board Of Patent Appeals And Interferences denying the request of the junior party Siemens/Patentee for reconsideration of the Board's February 22, 2010 Decision [Bd.R. 125 on motions]. Judgment was entered on February 23, 2010 by the Board for senior party Enzo/Applicants against junior party Siemens because the latter did not prevail on its threshold motions and it did not file a priority motion.

Pursuant to 37 C.F.R. §1.221(a), senior party Enzo/Applicants hereby request voluntary publication of the above-identified U.S. Patent Application Serial No. 08/479,995, filed on June 7, 1995.

§1.221(a) Voluntary publication or republication of patent application publication provides:

> Any request for publication of an application filed before, but pending on, November 29, 2000, and any request for republication of an application previously published under § 1.211, must include a copy of the application in compliance with the Office electronic filing system requirements and be accompanied by the publication fee set forth in § 1.18(d) and the processing fee set forth in § 1.17(i). If the request does not comply with the requirements of this paragraph or the copy of the application does not comply with the Office electronic filing system requirements, the Office will not publish the application and will refund the publication fee.

Pursuant to the above provisions of 37 C.F.R. §1.221(a), senior party Enzo/Applicants are submitting the following documents in connection with this publication request:

1. copy of U.S. Patent Application Serial No. 08/479,995, filed on June 7, 1995, in compliance with the Office electronic filing system requirements, including a listing of claims as amended on October 21, 2005 and allowed on November 21, 2005;[1]
2. $300.00 publication fee as set forth in 37 C.F.R. §1.18(d); and
3. $130.00 processing fee for taking action, i.e., requesting voluntary publication or republication of an application as set forth in 37 C.F.R. §1.17(i).[2]

Early and favorable action on this Request For Voluntary Publication of U.S. Patent Application Serial No. 08/479,995 is respectfully requested.

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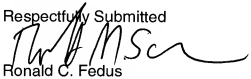
[1] The amendment filed October 21, 2005 was the last amendment filed in this application. The listing of claims accompanying this paper details the amendments filed in this application.
[2] Authorization is given below to charge the $300.00 publication fee and the $130.00 processing fee to senior party Enzo/Assignee's Deposit Account No. 05-1135.

SUMMARY & CONCLUSIONS

This paper is a Request For Voluntary Publication of U.S. Patent Application Serial No. 08/479,995, filed on June 7, 1995.

The fee for filing this Request is $430.00, based upon the $300.00 publication fee as set forth in 37 C.F.R. §1.18(d), and the $130.00 processing fee for taking action, i.e., requesting voluntary publication or republication of an application as set forth in 37 C.F.R. §1.17(i). Authorization is hereby given to charge the requisite $430.00 fee to Deposit Account No. 05-1135. No other fee or fees are believed due in connection with the filing of this Request. If any other such fee(s) are due, however, The Patent and Trademark Office is hereby authorized to charge the amount of any such fee to Deposit Account No. 05-1135, or to credit any overpayment thereto.

Respectfully Submitted



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TITLE OF THE INVENTION

ASSAY METHOD UTILIZING POLYNUCLEOTIDE SEQUENCES

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates to assays, both immunoassays and nucleic acid assays of analytes, which utilize a universal detection system based on polynucleotide interactions.

Description of the Prior Art

The analysis and detection of minute quantities of substances in biological and non-biological samples has become a routine practice in clinical and analytical laboratories around the world. Broadly, the analytical techniques can be divided into those based on ligand-receptor interactions (e.g., immunoassay-based techniques), and those based on nucleic acid hybridization (polynucleotide sequence-based techniques).

For example, immunoassay techniques involve, at some stage or step in the process, the non-covalent association between an antibody binding site and an antigen complementary therefor. See, for example, "An

Introduction to Radioimmunoassay and Related Techniques" by T. Chard, North Holland Publishing Company, Amsterdam, New York, Oxford, 1978. In polynucleotide sequence-based techniques, the process, at some step or another, involves the non-covalent binding of a polynucleotide sequence to a complementary sequence under hybridization conditions. (See for example, Falkow et al, U.S. Patent 4,358,535, Wahl et al, U.S. Patent 4,302,204, and Heimer, U.S. Patent 3,755,086.)

In a generalized sense, both the aforementioned techniques involve a primary recognition event, brought about by precise molecular alignment and interaction, and energetically favored by the release of non-covalent bonding free energy (e.g., hydrogen bonding, dispersion bonding, ionic bonding, dipolar bonding, and the like). In addition to the primary recognition event, both techniques also involve, at one step or another, a signalling event. This step or event relates to the necessity of detecting, in some demonstrable manner to a human or instrument detection system, the primary recognition event.

Signalling has been centered mainly in two broad areas: radioactive and non-radioactive techniques. Radioactive signalling has relied on radiolabeling of one or more components involved in the system, with

such atoms as ^{32}P, ^{131}I, ^{14}C, ^{3}H, and the like. Detection is usually by means of a radioactivity detector. Non-radioactive techniques have been increasingly used in the last few years, since they involve no radioactivity, thus making such techniques safer, cleaner and more stable towards storage. They have been developed to sensitivities as high if not higher than radiolabeling techniques. Among the most common non-radioactive signalling techniques used at present are enzyme linked immunoassays (see, for example, Schuurs, A.H. et al, Clinica Chimica Acta, 81: 1-40 (1977)), fluorescence (Bauman et al, Chromosoma, 84: 1-18 (1981)), indirect immunofluorescence (Rudkin et al, Nature, 265: 472-473 (1977)), avidin-biotin interactions (Manning, J, et al, Biochemistry, 16: 1365-1370 (1977)), electron microscopy of electron dense nuclei such as ferritin (Broker , T.R. et al, Nucleic Acids Research 5: 363-384 (1978)), latex attachment (Sodja, A., ibid 35: 385-401 (1978)), combinations of the aforementioned techniques, and others.

The primary recognition event and the signalling event need to be coupled to each other, directly or indirectly, proportionately or inversely proportionately. Thus, in such systems as nucleic acid hybridizations with radiolabeled probes, the amount of

radioactivity is usually directly proportional to the amount of analyte present. The same is true with a system such as a sandwich immunoassay, wherein the amount of labeled second antibody being detected is normally directly proportional to the amount of antigen present in the sample. Inversely proportional techniques include, for example, competitive immunoassays, wherein the amount of detected signal decreases the more analyte present in the sample.

The prior art has also utilized amplification techiques, wherein the signalling event is related to the primary recognition event in a ratio greater than 1:1. Thus, the signalling component of the assay may be present in a ratio of 10:1 to each recognition component, thereby providing a 10-fold increase in sensitivity.

The great versatility of polynucleotide sequence-based recognition systems has caused an extensive amount of experimentation and research to be invested therein. This versatility is brought about by the precise alignment of complementary nucleotide bases to each other, adenine (A) aligning to thymidine (T) and guanine aligning with cytidine (C). Given this complementarity, it is possible to utilize any desired sequence to provide an infinitely versatile system.

One of the impediments to a more extensive use of polynucleotide interaction-based systems, however, has been the necessity of attaching signalling or reporter groups (such as radioactive phosphorous, or enzymes, or biotin, or the like) to individual nucleotide residues in the polymer chain. At least two problems arise out of this requirement.

First, the chemical reaction conditions involved in the modification of a polynucleotide polymer are generally too vigorous to be sufficiently selective for any one nucleotide in particular. For example, dicarbonyl reagents such as kethoxal or glyoxal will indiscriminately react with guanine (see for example Shapiro, R. et al, Biochemistry, 5: 2799-2807 (1966), Litt, M, ibid, 8: 3249-3253 (1969), or Politz, S.M. et al, ibid, 20: 372-378 (1981)). Thus, if one were to use a dicarbonyl-based cross-linking agent to attach an enzyme or a low molecular signalling compound directly on a polynucleotide chain, one would risk (and in fact one obtains) modification of a substantial amount of all guanine residues in the chain. This, of course, severely hinders the use of such modified chain in a recognition step. This problem has been solved in the prior art by the use of enzymatic (DNA polymerase-based) incorporation of individual modified nucleotides (previously modified in a non-hydrogen-bond-disruptive

manner) into a nascent polynucleotide chain. It would, however, be preferred to utilize chemical modification techniques on the final polynucleotide polymer itself.

A second problem is associated with the attachment of signalling groups to polynucleotides and is somewhat related to the first. The problem is based on the necessity of synthesizing, by sometimes sophisticated and elaborate synthetic techniques, the modified monomeric nucleotide units themselves, prior to their enzymatic incorporation into polymer. Thus, radiolabeled nucleotides or biotin-labelled nucleotides have to be independently synthesized. Further, the amount of incorporation of a chemically modified nucleotide into final nucleic acid polymer may also influence the ability of a probe to recognize a given sequence on the analyte. This is particularly important if amplification techniques are utilized wherein signalling groups greatly outnumber recognition groups.

It would therefore be very useful to develop an assay system which utilizes components that are easily prepared, amenable to chemical modification rather than enzymatic-based reactions, that would utilize the great versatility of polynucleotide-based sequence recognition, and include the possibility of signal amplification methods.

SUMMARY OF THE INVENTION

The present invention provides a universal assay system which takes advantage of polynucleotide sequence recognitions, which allows for the use of chemical modification reactions, which is also capable of utilizing recognition events based on any type of non-bonding interaction, and which can use any of the myriad of available signalling methods.

The process of the invention comprises a method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises:

providing a molecular bridging entity (B) having thereon

(i) a portion capable of recognizing said molecularly recognizable portion on said analyte; and

(ii) a portion comprising a polynucleotide sequence; and

a signalling entity (C) having thereon

(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity, thereby to form

a stable polynucleotide hybrid,

and

(ii) a signal generating portion;

forming a complex comprising:

(1) said analyte (A) complexed through said molecularly recognizable portion to

(2) said recognizing portion of said entity (B); said entity (B) being complexed through said polynucleotide portion thereon to

(3) said polynucleotide portion of said signalling entity; and

detecting a signal by means of said signal generating portion present in said complex.

The invention provides, in addition to the aforementioned process, various elements and components to be used therein, such as various molecular bridging entities, and various signalling entities, as well as kits comprising said entities, and other components for use in the process.

In essence, the invention is based on the realization that the recognition portion and the signalling portion of the multi-component assay system should be present on different components of the system, thereby separating them, and avoiding the

interference of the signalling portion on the recognition portion. This separation into multi-component entities, also allows the signalling portion to be attached to one of the components by chemical modification techniques, without affecting the recognition component.

Uses for the process, system and components are unlimited, and include all of the uses to which prior art assay techniques have been put, as well as generally, the detection of any analyte capable of recognition, in any sample.

BRIEF DESCRIPTION OF THE FIGURES

The invention will be better understood by reference to the attached Figures wherein:

FIGURE 1 represents a generalized scheme for the assay system of the invention. Analyte 1, having a molecularly recognizable portion 2 thereon, is brought into contact with molecular bridging entity 3, having a portion 4 thereon capable of recognizing the, molecularly recognizable portion 2 on analyte 1. Bridging entity 3, in addition, carries a portion 5 comprising a polynucleotide sequence, generally denoted as ATCGATC... . Also present in the system is signalling entity 6 having thereon a polynucleotide portion 7 capable of annealing to polynucleotide

portion 5 of the bridging entity 3. The signalling entity 6 also carries a signal generating portion 8. When analyte is present in the sample being analyzed, interaction occurs with bridging entity 3 through the recognizable and recognition portions 2 and 4, respectively. The complex formed thereby is then annealed through the polynucleotide portion 5 to the complementary polynucleotide portion 7 on the signalling entity, which brings the signalling portion 8 into some stoichiometric relation with the analyte 1.

FIGURE 2 shows a preferred system under the broader concept of the invention, wherein analyte 9 comprises a DNA sequence 10 (generally indicated as ATCGATCGATC). Bridging entity 11, shown as a single-stranded circular polynucleotide polymer, carries a recognizing portion 12 which is a DNA sequence complementary to the DNA sequence of the analyte. Bridging entity 11 also carries, in addition, a poly G sequence 13, which is capable of annealing and forming a stable hybrid with complementary poly C sequence 15 on signalling entity 14. Signalling entity 14 also carries a biotin portion 16 as its signal generating group. Presence of the DNA sequence 10 in the sample being analyzed causes the bridging entity 11 to hybridize thereto, and subsequent annealing of the signalling entity to the thus formed complex attaches

the biotin portion, through the network, to the analyte. The biotin portion 16 can then be detected, for example by addition of an avidin/enzyme couple, followed by addition of enzyme substrate, and color detection.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

SYSTEM COMPONENTS

The term "analyte" as used in the specification and claims includes any substance or substances either alone or in admixtures, which presence is to be detected and, if necessary, quantitated. The analyte may be a molecule of small or high molecular weight, a molecular complex, or a biological system, such as a virus, a cell, or group of cells. Among the common analytes are proteins, polysaccharides, lipopolysaccharides, protein complexes, nucleic acids or segments thereof, either single- or double-stranded, whole viruses or viral components such as cores or capsids, bacteria of various different types, tissue cells, and the like. Among the most common proteins are the structural proteins, enzymes, immunoglobulins, or fragments thereof. Among the most common nucleic acids are DNA and RNA of various different types, such as tRNA, mRNA, rRNA, and the like. Bacteria, either whole or fragments thereof, such as cell walls or other

recognizable portions, include both gram positive and gram negative bacteria. Fungii, algae, and other submicroscopic microorganisms are also included, as well as animal (e.g., mammalian) cells.

The analyte should have a "molecularly recognizable portion" thereon. This phrase denotes any molecular portion of the analyte which is capable of being recognized by a complementary molecular portion on the bridging entity of the system. Molecular recognition, as will be understood by those of skill in the art, includes the non-covalent binding in three dimensions between complementary portions of two molecules. A molecularly recognizable portion on an analyte may be, for example, a polynucleotide sequence, such as RNA or DNA, to be recognized by its complementary sequence; an antigen portion, to be recognized by its corresponding monoclonal or polyclonal antibody; an antibody portion, to be recognized by its corresponding antigen; a lectin portion, to be recognized by its sugar; a sugar portion, to be recognized by its lectin; a hormone portion, to be recognized by its receptor; a receptor portion, to be recognized by its hormone; an inhibitor portion, to be recognized by its enzyme; an enzyme portion, to be recognized by its inhibitor; a cofactor portion, to be recognized by a cofactor enzyme binding

site; a cofactor enzyme binding site portion, to recognized by its cofactor; binding ligand recognized by its substrate and vice versa (i.e. biotin-avidin); or any permutation or combinations thereof.

Among the most common molecularly recognizable portions are the three-dimensional protein arrangements in antigens of various different sorts, the cell wall structures present in various cells, or the nucleic acid sequences present in the DNA or RNA of organisms.

The second component of the system is the "molecular bridging entity". This entity need only contain a first portion capable of recognizing the molecularly recognizable portion on the analyte, and a second portion which comprises a polynucleotide sequence. These two portions of the bridging entity may be of the same type (i.e., both of them polynucleotide sequences, albeit different ones) or of a different type (one being, for example, an antibody portion and the other the polynucleotide portion.)

The portion on the bridging entity capable of recognizing the molecularly recognizable portion on the analyte must contain a molecule or molecular fragment complementary to the recognizable portion on the analyte. Therefore, if the analyte contains a polynucleotide sequence, the recognizing portion of the bridging entity should be a complementary

polynucleotide sequence or "probe". If the molecularly recognizable portion on the analyte is a generalized antigen, the recognizing portion on the bridging entity should be an antibody thereto. The same is true with respect to the complementary pairs sugar/lectin, receptor/hormone, inhibitor/enzyme, and the like, described previously.

The second portion of the molecular bridging entity must comprise a polynucleotide sequence. The polynucleotide sequence can be any chosen sequence, provided that it is long enough to provide stable annealing with a complementary sequence under given stringency conditions, that it be complementary to the polynucleotide sequence on the signalling entity, and, if the recognizing portion on the bridging entity is itself a polynucleotide sequence, that it be sufficiently different from said recognizing sequence portion, to avoid hybrid formation between the analyte sequence and the second polynucleotide portion on the bridging entity. The latter of the three conditions is required to prevent molecular confusion with concommitant appearance of false results.

The second portion polynucleotide sequence on the bridging entity (i.e., the one complementary to the sequence on the signalling entity) may code for a particular gene product or products, or may code for no

gene product at all. Thus, any structural gene or portion thereof could be used as the polynucleotide sequence portion on the bridging entity. A preferred sequence, however, would not code for a given gene since such coding may interfere with complementary gene sequences present in the analyte. It is thus preferred to choose polynucleotide sequence portions on the bridging entity which are non-coding, and not likely to be complementary to sequences on the analyte such as, for example, sequences comprising poly deoxy G, poly deoxy A, poly deoxy GT, poly deoxy GA, poly deoxy GAT, poly deoxy GTA, or any other low complexity (repeating) sequence. By "polynucleotide" is meant to include both polyribonucleotides, polydeoxyribonucleotides, or any poly-purine, -pyrimidine or analog and combinations thereof.

Specific examples of bridging entities as used in this invention are covalently attached entities of monoclonal or polyclonal antibodies with polynucleotides, polynucleotides with polynucleotides, protein antigens with polynucleotides, saccharides with polynucleotides, small molecular weight organic compounds with polynucleotides, lectins with polynucleotides, receptors with polynucleotides, hormones with polynucleotides, enzyme inhibitors with polynucleotides, enzyme cofactors with polynucleotides, and combinations and permutations thereof.

The molecular ratio of the recognizing portion on the bridging entity, to the polynucleotides sequence portion thereon need not necessarily be 1:1. There may be many more polynucleotide sequence portions than recognizing portions, or vice versa. In the case when the ratio of polynucleotide sequence portion to recognizing portion on the bridging entity is greater than 1, for example, 5, 10 or greater, the system amplifies the primary recognition event by a factor equal to the ratio.

Among preferred bridging entities of the invention are circular polymers of single- or double-stranded DNA. The single-stranded ones include so-called filamentous phages, such as fd, f1 and M13 (see Van Wezenbeek, P., Gene, 11: 129 (1980).) These filamentous phages do not lyse their host; rather, they are released from infected cells as the cells continue to grow and divide. M13 is commercially available (Bethesda Research Labs, Inc.) and has been extensively used as a cloning and sequencing system. It can be cut at a restriction endonuclease site to incorporate therein any desired polynucleotide probe sequence, to serve as the recognizing portion of the bridging entity. Either at the same site or at a different site, the circular DNA can be opened to incorporate the polynucleotide portion of the bridging entity, capable

of annealing to the complementary portion on the signalling entity. In this manner, a bridging entity is obtained which is capable or recognizing a gene sequence on an analyte by hybridization, and is also capable of annealing to the signalling entity through another sequence thereon. (A generalized system of this sort is shown in FIGURE 2.)

In one particularly preferred embodiment, the bridging entity comprises a DNA polymer which carries the sequence for a given gene (for example, a viral probe such as Hepatitis B virus, EBV and the like), and, at another place in the polymer, a poly G, or poly GT, or poly dG, or poly dC, or poly dCA, or poly dGdT polynucleotide portion. Ideally, a single-stranded DNA polymer can be provided carrying the polynucleotide portion capable of annealing to the signalling entity (e.g., poly dGT), and also carrying a restriction endonuclease site, so that the user can incorporate any desired DNA probe thereinto. In this manner, by a few simple enzymatic manipulations, the DNA polymer bridging entity can be quickly transformed into a wide variety of bridging entities.

The signalling entity of the invention needs to carry both a polynucleotide portion capable of annealing to the complementary portion on the bridging entity, and a signal generating portion.

The polynucleotide portion on the signalling entity is defined by the same parameters as the complementary portion on the molecular bridging entity. It should be of a length capable of forming stable polynucleotide hybrids with the corresponding polynucleotide on the bridging entity. "Annealing" as used in this part of the invention refers to the required base pair matching between two complementary polynucleotide strands, under any given set of stringency conditions. It is generally understood in the art that about 12 to 13 nucleotides in a row are necessary for stable annealing. Thus, as a minimum, the number of nucleotides in the sequence should be that necessary for stable annealing with the polynucleotide portion of the bridging entity. The formation of the hybrid should be stable enough to withstand any washing, elution, or signal detection procedures which follow hybridization.

The "signal generating" portion of the signalling entity can encompass virtually any of the signal generating systems used in the prior art, and any system to be developed in the future. It comprises a moiety which generates a signal itself (e.g., a radiolabel), or a moiety which, upon further reaction or manipulation will give rise to a signal (e.g., an enzyme-linked system). Both types are herein called "signal generating" portions.

Thus, the signal generating portion may comprise a radiolabel (e.g., ^{14}C, ^{32}P, ^{3}H, and the like), an enzyme (e.g., peroxidase, alkaline or acid phosphatase, and the like), a bacterial label, a fluorescent label, an antibody (which may be used in a double antibody system), an antigen (to be used with a labeled antibody), a small molecule such as biotin (to be used with an avidin, streptavidin, or antibiotin system), a latex particle (to be used in a buoyancy or latex agglutination system), an electron dense compound such as ferritin (to be used with electron microscopy), or any combinations or permutations thereof.

For example, if the signal generating portion of the signalling entity is an antigen, a signal can be generated by complexing said antigen with an antibody/enzyme conjugate, followed by addition of enzyme substrate. If the signal generating portion of the signalling entity were an antibody, signal can be generated by complexing anti-antibody or an F_c binding protein such as Protein A therewith, which second antibody or Protein A have been conjugated to an enzyme.

Among the preferred signal generating portions are those based on the biotin/avidin system. This system can be incorporated into the signalling entity by a variety of means. For example, the polynucleotide

portion of the signalling entity can be covalently attached to biotin via a cytochrome c bridge (Manning et al, Biochemistry, 16: 1364-1370 (1977), Manning et al, Chromosoma, 53: 107-117 (1975), Sodja, A., Nucleic Acids Research, 5: 385-401 (1978)), or the biotin can be covalently incorporated into specific nucleotide residues (Langer, P.R., Proceedings of the National Academy of Sciences, USA, 78: 6633-6637 (1981)), or the biotin can be attached to a polynucleotide by means of a diamine (e.g., pentane diamine) bridge (Broker, T.R., et al, Nucleic Acids Research 5: 363-384 (1978)). Interaction of the biotin molecules in the signal generating portion with avidin, streptavidin or anti-biotin antibodies is then carried out, wherein the avidin, streptavidin or the antibodies are conjugated to such signalling components as latex particles (Sodja, A., et al, supra, or Manning, et al Chromosoma, supra), ferritin (Broker, supra), a fluorogen such as fluorescein, an enzyme, or the like.

A thorough description of various non-radioactive signal generating systems, both biotin/avidin-based and non-biotin/avidin-based can be found in two presently copending patent applications: Serial Number 255,223, filed at the U.S. Patent and Trademark Office on April 17, 1981 to "Modified Nucleotides and Methods of Preparing and Using Same" by Ward et al, and Serial

Number 391,440, filed on June 23, 1982 at the United States Patent and Trademark Office to "Modified Nucleotides, Methods of Preparing and Utilizing, and Compositions Containing the Same" by Engelhardt et al, both of which are herein fully incorporated by reference.

In addition, the signal generating portion of the signalling entity need not be a polynucleotide which has been chemically modified or artificially altered in any way. Some biological systems perform in vivo modifications which can be utilized by this sytem. One such system is the phage T_4 grown in E. coli. T_4 DNA has a very high content of glycosylated C residues. It is possible to insert (clone) a low complexity repeating polynucleotide sequence into phage T_4. This phage would then be naturally propagated and glycosylated in the host. The viral DNA can be isolated from E. coli and bound to a complementary sequence on the bridging moiety. Detection could then be accomplished via a lectin/enzyme system, or lectin/fluorescent dye, or lectin/electron dense material, or lectin/radioactive label, using the natural glucose residues on the T_4 DNA as points of anchorage. Other T (even) phages such as T_2, T_6, or T_8 can also be used.

The number of signal generating portions need not have a 1:1 stoichiometry with the number of polynucleotide portions on the signalling entity. When the ratio of signal generating portions to polynucleotide portion in the signalling portion of the signalling entity is greater than 1 (e.g. greater than 5, or greater than 10), the system functions as an amplification system. Thus, for example, if there are 10 signal generating portions per polynucleotide portion in the signalling entity, a 10:1 signal amplification over the bridging entity is obtained. If, in addition, the bridging entity has a signal amplification system itself, i.e., the ratio of polynucleotide portions to recognizing portions on the bridging entity is greater than 1, the overall signal amplification system is the product of both ratios. This means that for every primary recognition event occurring at the level of analyte, the amplification quickly increases and leads to very sensitive systems. This factor can be readily controlled by the design of the system components.

PROCESSES OF PREPARATION

The bridging entity, as stated previously, needs to comprise a recognizing portion and a polynucleotide portion. The signalling entity requires a

polynucleotide portion and a signal generating portion. Thus, generally, the method of preparation of individual components in the system will relate to the covalent attachment of polynucleotides, or individual components thereof, to 1) protein moieties, 2) saccharide moieties, 3) other polynucleotide moieties, 4) small molecular weight compounds (e.g., MW less than about 1000), 5) radiolabels, or 6) insoluble phases such as bacterial particles, or latex particles. Therefore, the chemistry involved in the covalent attachment or conjugation of nucleic acids to their corresponding partner or partners is well within the skill of the art.

The covalent attachment of polynucleotide sequences to proteins is well described in the literature. Normally, the reaction is carried out directly by carbodiimide crosslinking (Halloran, M.K. J. Immunol. 373 (1966) or by cross-linking the protein to the nucleic acid in the presence of such agents as formaldehyde (see e.g., Brutlag, D. et al, Biochemistry, 8: 3214-3218 (1969), Manning, J.E., et al, Chromosoma, 53: 107-117 (1975)), (4-azidophenyl) glyoxal (Politz, S.M., Biochemistry, 20: 372-378 (1981)); by oxidation of 2',3'-hydroxy ends of a polyribonucleotide, followed by i) Schiff base formation with the amine groups of a protein, and by

ii) borohydride reduction (Sodja, A., et al, Nucleic Acids Research, 5: 385-401 (1978)). Other methods include direct bromination of DNA (Jones, A.S., Nature 183: 1603 (1959) followed by reaction with diaminohexane (Lowe, C.R., Eur. J. Biochem. 73: 265-274, (1977)), and coupling via protein carboxyl functions; or by mercuration of cytosine moieties (Dale, R.M.K. et al, P.N.A.S., 70: 2236-2242, (1973)) followed by halogenation (Dale, R.M.K. et al, Nucleic Acids Res. 2:915-930 (1975)), reaction with diaminohexane and coupling to protein carboxyl groups.

Of particular interest is the use of dicarbonyl reagents for chemical modification of guanine bases in the preparation of the signalling entity. This represents one of the particularly useful advantages of the present multi-component assay system. If the polynucleotide portion on the signalling entity has very low G content, it is possible to chemically react said polynucleotide portion with any material via a cross-linking agent such as a dicarbonyl compound, without fear of irreversibly modifying the annealing properties of the polynucleotide portion in question. This applies equally well to the attachment of any small molecular weight molecule to the polynucleotide portion, which attachment depends on the use of dicarbonyl compounds, or other nondiscriminating cross-

linking agents. This technique saves the effort and time involved in previously modifying individual nucleotide residues, and then incorporating these into a polynucleotide strand by enzymatic polymerization.

The attachment of polynucleotide sequences to saccharides can be carried out according to Cramer et al, Chem. Ber 92: 384-391 (1959). Saccharides having up to 20 saccharide units are preferred.

The attachment of polynucleotide sequences to other polynucleotide sequences is carried out by either chemical or enzymatic techniques, such as using blunt end ligation or ligation based on the presence of cohesive terminii generated by endonuclease digestion enzymes. The cleavage and ligation of DNA sequences to each other is well described in Helling and Lomax, "The Molecular Cloning of Genes-General Procedures" which is Chapter 1 of "Genetic Engineering" by Chakrabarty, CRC Press, 1978, pages 1-30.

Other methods for attaching polynucleotides to polynucleotides include using SS Dna + Ribo dUTP + Terminal Transferase (Roychoudery, R. + Wu, R., in Meth. in Enz., LXV, 43, (1980)); Periodate oxidation, reductive amination with amino derivatives including 1,6 diamino hexane (1), 3-aminopropionic acid (2), or bis (2-amino ethanethiol) (3), (Perikeh, I Mach, S, and Cuatrecasas, in Meth. in Enz. XXXIV, 82 (1974)); or by

limited bromination of C (through mercuration) (Dale & Ward supra) and subsequent reaction of DNA with same reagents ((1), (2) + (3)).

DNA derivatives of compounds (1) or (2), above, can subsequently be coupled to proteins via water-souble carbodiimide derivatives (Inman, J.K. in Meth in Enz., XXXIV, 52-53) (1974). In case (3), the protein can be activated with the N-hydroxy succinimide ester of bromoacetic acid. The resulting activated protein can be covalently linked to the thiolated nucleic acid at room temperature.

The covalent incorporation of radiolabels such as ^{32}P into DNA sequences can be done by any of a variety of methods, such as direct incorporation of radiolabeled nucleotides by enzymatic polymerization, nick translation, and the like (Rigby et al, J. Mol. Biol. 113: 237-251 (1977).)

The preparation of the individual elements of the signal generating system such as protein/latex conjugates, protein/ferritin conjugates, antibody/enzyme conjugates, fluorogen/antibody conjugates, avidin/enzyme conjugates, and the like is generally well known in the art and will be not described in further detail.

The specific preparation of individual polynucleotide sequences is also well understood by

those of skill in the art. For example, if a polynucleotide sequence comprises a gene or genes, the same can be prepared by synthetic procedures, or can be prepared by reverse transcription of mRNA using reverse transcriptase to generate a complementary DNA. If the polynucleotide sequence comprises a strand of any one nucleotide (e.g., poly dG or poly dC) or a strand of any dinucleotide pair (e.g., poly dGT, or the like), the same can be readily prepared by enzymatic-based reactions such as by using DNA polymerase, or by synthetic methodology.

METHODS OF USE

The analyte being detected can be present in any biological or non-biological sample, such as clinical samples, for example, blood, urine, feces, saliva, pus, semen, serum, other tissues, fermentation broths, culture media, and the like.

If necessary, the analyte is preextracted or purified by methods known to concentrate the particular type of analyte from its admixing components. For example, if the analyte is a protein or protein-containing fraction, protein extraction procedures such as salt precipitations, alcohol precipitations or chromatography can be utilized. If the analyte comprises a nucleic acid segment to be identified,

nucleic acid extraction procedures, such as phenol extraction, can be utilized. The analyte, together with impurifying materials if such be the case, can be tested in the mixture as purified or, especially when it is a nucleic acid segment, can be immobilized (see for example, Wahl et al U.S. Patent 4,302,204.)

The composition suspected of containing the analyte is incubated with the bridging entity for a time and under conditions sufficient to allow complexation between the recognizable portion of the analyte and the recognizing portion on the bridging entity. These conditions will vary depending on the nature and amount of the analyte and of the bridging entity. Normally, after complexation has occurred, the sample is washed with neutral solution to remove excess bridging entity. Alternatively, no wash is carried out at this stage but signalling entity is added to the mixture and a wash is carried out after annealing has occurred between the polynucleotide strands on the bridging entity and on the signalling entity respectively. Hybridization of the bridging entity strand to the signalling entity strand is carried out under hybridizing conditions and under any set of stringency conditions. A final wash may be necessary prior to generation of signal.

Signal generation is carried out by any given technique, depending on the nature of the signal generating system. Thus, if an enzyme linked assay is utilized, the ternary complex between analyte, bridging entity and signalling entity is allowed to incubate with the enzyme carrying reagent (e.g., enzyme/antibody conjugate), and substrate is added thereto to develop color. Alternatively, enzyme might be attached directly to the polynucleotide strand on the signalling entity, in which case substrate is added immediately thereafter to obtain color development. If the signal generating portion of the signalling entity is a biotin moiety, then a biotin reactive molecule such as avidin, streptavidin or anti-biotin antibody, is added thereto. The biotin reactive molecule is conjugated to an enzyme, a fluorescent compound, an electron dense compound, or an insoluble solid phase, and detection is carried out by appropriate means.

APPLICATIONS

The applications of the system of the invention are unlimited. Any analyte desired to be detected and analyzed in any sample can be subject to the method of the invention.

For example, the system can be used for microorganism detection and identification, by using

any of a variety of recognizable portions and recognizing portions in the analyte and the bridging entity respectively.

Of particular interest is the detection and identification of viral and bacterial DNA sequences.

The method can be utilized to diagnose genetic disorders by preparing a polynucleotide complementary to a DNA gene sequence which is associated with the genetic disorder, and detecting the presence of any primary recognition events. Among these genetic diseases, for example, can be mentioned thalassemia. The determination of thalassemia can be made (for known genetic defects) by hybridization of oligonucleotides to genomic DNA followed by specific washing procedures or by restriction analysis and Southern, Northern, or Dot blots.

Another use for the system of the invention is in chromosomal karyotyping, which comprises using a series of modified polynucleotides corresponding to a series of defined genetic sequences located on chromosomes, and then detecting primary recognition events thereon.

Another use includes a method for identifying or locating hormone receptor sites on the surface of cells, which comprises binding a hormone receptor binding compound present in the bridging entity to the

receptor site, and then detecting primary recognition events by means of the signalling system of the invention.

Another use comprises the detection of cancer, by detecting in the blood or serum of suspect subjects, the presence of cancer associated antigens such as CEA (carcinoembryonic antigen). Another use includes a method of tumor or cancer cell identification or detection which comprises identifying malignant cells by detecting the absence of normal receptors sites by the technique of the invention.

Another use includes a method of detecting antibodies against certain infectious diseases in animals, by using antigen therefor as a recognizing portion in the molecular bridging entity. Sugar levels or differential glycosylated hemoglobin levels can be detected in diabetes by using a lectin as the recognizing portion on the molecular bridging entity.

Yet another use for the process and system of the invention is in the insolubilization of analytes. Thus, if a sample is suspected of containing an analyte, and one wishes to extract and purify the analyte from the sample, the "signalling entity" is designed so that the signal generating portion comprises or is capable of specifically binding to an insoluble solid phase, such as a natural or synthetic

aqueous insoluble resin, a glass, a plastic such as an acrylate or methacrylate, the inside of a test tube wall, or of a well, and the like. The bridging entity is allowed to incubate with the solid phase, thus creating recognition sites (i.e., affinity surfaces) for the analyte, which is then bound thereto.

The present invention lends itself readily to the preparation of kits comprising one or more of the elements necessary to perform the detection and identification process. Thus, a kit may comprise a carrier being compartmentalized to receive in close confinement therein one or more container means or series of container means such as test tubes, vials, flasks, bottles, syringes, or the like. A first of said container means or series of container means may contain the bridging entity, for recognition of any of a wide variety of analytes. A second container means or series of container means may contain signalling entities. A third container means or series of container means may contain predetermined amounts of analyte, so as to provide the ability to construct a standard curve into which results can be interpolated. Other container means or series of container means may contain the elements necessary to generate the signal, such as enzyme linked conjugates, avidin linked conjugates, ferritin linked conjugates,

latex linked conjugates, fluorogen linked conjugates, and the like.

In a preferred embodiment, the kit carrier contains a first container means comprising a bridging system which is DNA carrying a polynucleotide portion of predetermined sequence and a restriction site or cleavage site on the DNA which can be used to incorporate any of a number of gene probes for testing and identifying genetic sequences associated with the analyte. Another container means in this preferred kit would comprise a signalling entity carrying a polynucleotide portion complementary to the polynucleotide portion present in the DNA present in the first container means, and a signal generating portion which may be any of the aforementioned systems. A third container means or series of container means in this preferred kit may comprise a variety of DNA probes complementary to the genetic sequences present on one or more polynucleotide-containing analytes such as viruses, bacteria, cells and the like.

Thus, the user would utilize a cleavage method (such as use of a restriction endonuclease) to open the DNA in the first container, incorporate thereinto any desired DNA probe present in the third container or container series, ligate the polymer and then utilize

the bridging entity and the signalling entity to detect and identify the presence of any desired genetic sequence present in the analyte. It should be kept in mind that a single strand cannot be cut with a restriction enzyme unless a linker (which spans the site) is first hybridized to it, thereby creating a double-strand in that location. Normally the gene would be ligated into the RF (double-stranded) so that it could be amplified in a microorganism.

Having now generally described this invention, the same will be illustrated by reference to certain specific embodiments which are included herein for purposes of illustration only and are not intended to be limiting unless otherwise specified.

Examples

Examples 1-31 relate to processes of preparation of bridging and signalling moeties. The examples show preparation methods which may be classified within the following categories:

1) Chemical activation of oligonucleotides for subsequent coupling to proteins, saccharides and small molecules.

2) Chemical activation of proteins for subsequent coupling to DNA, saccharides and small molecules.

3) Chemical activation of saccharides for subsequent coupling to DNA, protein and small molecules.

4) Chemical activation of small molecules for subsequent coupling to DNA and protein.

5) Coupling of DNA to protein, saccharides and small molecules.

The examples classified within the above categories are as follows:

1) Chemical activation of Oligonucleotides.

A. By terminal ribonucleotide labelling followed by periodic oxidation and reductive amination: Examples 11, 12;

B. By non-specific bromination: Examples 28, 29, 30.

C. By specific activation of cytosine moieties via 5-iodocytosine: Examples 16, 17 18.

D. By specific activation of guanosine moieties via reaction with 3, 4, 5-trichlorodiazobenzene: Example 1.

E. By specific activation of adenosine and guanosine-moieties via reaction with 2,3-dibromopropanal: Example 9.

2) Chemical Activation of proteins

A. By bromoacetylation: Examples 13, 14.

3) Activation of saccharides

A. By activation of reducing saccharides: Examples 4, 5, 6.

B. By activation of non-reducing saccharides: Examples 7, 8.

4) Activation of small moieties

A. Biotin: Examples 2, 33, 23, 24, 25, 26

B. DCTA: Example 3.

5) Coupling of DNA to protein, saccharides and small molecules

A. To protein: Examples 15, 19, 20.

B. Saccharides: Example 19, 18.

C. To small molecules: Examples 19, 10, 21, 27.

Example 1

Activation of DNA with 3,4,5-Trichloraniline

100 mg of 3,4,5-trichloroaniline were dissolved in 2.5 ml of 0.5M HCl in 50% DMSO and cooled on ice, under vigorous stirring, an equimolar amount of $NaNO_2$ from a cold 1M solution were added, as rapidly as possible, and then stirring was continued for 10 minutes. 1 mg of 3H or fd DNA in 300 µl of water were mixed with 300 µl of 2M cacodylate buffer pH 6,6 and 500 µl DMSO. (By addition of DMSO the pH of the solution rises to 8.3). 20 µl of the freshly prepared diazonium solution were added thereto and the mixture was

incubated for two hours at room temperature. The slight precipitate which appeared during the incubation was removed by centrifugation. The solution was then made 0.4 M with ammonium acetate and the DNA was precipitated with ethanol.

Example 1a

Reaction of Trichloroaniline-activated DNA with thiols. Example of Reaction with DCTA-SH and thiol activated mannose

Pd DNA activated with 3,4,5-Trichloroaniline (Example 1) was dissolved in 0.1M sodium hydroxide with an equal amount of 0.1M K_2HPO_4. This solution was treated with an equal volume of 0.1M DCTA-SH (Example 3) or thiol activated mannose (Ex. 6 and 9), and incubated under argon at 65° for 2 hours. The precipitated disulfides were removed by centrifugation and the DNA was purified by G50 chromatography and stored at -20°C. Using radioactive Ni to level the derivatized DNA, it was determined that 60% of guanines had been labelled.

Example 2

Biotin-SH

Three milimoles of Biotin -NHS ester were dissolved in 25 ml of anhydrous DMF and mixed with a 1M solution of cysteamine hydrochloride in 12 ml of 0.5M

sodium bicarbonate and the mixture was incubated at room temperature overnight. During the incubation a heavy precipitate appeared. The liquid was removed under reduced pressure at 45°C and the residue was suspended in 50 ml absolute ethanol, 1 g of $NaBH_4$ was added and the suspension was stirred for one hour at 75°C. The ethanol was removed and cold 1 M HCl was added to bring the pH to 4.5, and the water was removed under reduced pressure at 35°C. (All these operations were performed under an argon atmosphere to prevent oxidation of the thiol.) The solid residue was powdered and triturated with 4 ml of cold deareated 0.01 M acetic acid. These procedure was repeated twice and the residue was lyophilized. TLC chromatography showed that the main biotin spot contained thiol; two minor spots were thiol negative. In all reactions the amount of biotin used was based on the thiol content.

Example 3

DCTA-SH

One milimole of DCTA-bromide was added to 5 ml of 50% DMF containing 0.2 ml of 2,3-dithioethylene and 0.5 ml of triethylamine. The mixture was incubated under argon for 2 hours at 60-70°C. The solution was then mixed with 20 ml of water and loaded onto a Dowex AG-1 column of 9 ml bed volume. The column was washed with

50 ml of 0.1M acetic acid solution until the flowthrough was thiol free. The DCTA-SH was then eluted with 0.25M HCl. The thiol containing fractions were combined, evaporated to dryness under reduced pressure at 40°C and the free acid (300mg) was stored at -20°C under argon.

Example 4

1-O-Methyl-6-O-Tosyl-α-D-mannopyranoside

Non-reducing saccharides were activated through the primary alcohol group by forming the tosylate, and displacing it with ammonia to form an amino group, or with a dithiol to form a thiol group. An example is described here, the activation of α-methyl-d-mannoside, a non-reducing sugar and of mannose as a reducing one. The tosylation was performed analogous to a published procedure (F. Cramer et al. Chem. Ber. 92, 384-391 (1979).)

23 g of methyl-D-mannoside were dissolved in 400 ml of absolute pyridine and the solution was cooled to -15°C on an ice salt mixture. A solution of 24.6 g of p-Toluene sulfonyl chloride in 80 ml absolute pyridine was added to the vigorously stirred mixure and reacted at -15°C for 30 minutes and 12 hours at 20°C. The pyridine was removed under reduced pressure at 40°C and the residue was dissolved in chloroform. The solution

was warmed to 50°C and washed successively with 0.5 M potassium hydrogen sulfate followed by 0.5M potassium bicarbonate solution at 50°C (the 50 degree temperature was necessary to avoid gel formation).

Example 5

6-amino- α -methyl-D-mannoside hydrochloride

A solution of 6 g of the tosylate (Example 4) in 130 ml absolute methanol was saturated at 1°C with dry ammonia and autoclaved for 16 hours at 120°C. The dark reaction product was refluxed with charcoal and methanol was removed by distillation leaving a slight yellow syrup. The syrup was dissolved in water and the sulfonate liberated during the displacement reaction was removed by passing the solution through an anion-exchanger. HCl was added to the elutate to bring the pH to 5.0 and the water was removed under reduced pressure at 40°C. The residue was triturated with a mixture of 15 ml of absolute methanol and 15 ml of absolute ether and the solid material was dissolved in 50 ml of absolute methanol and cooled, the addition of 25 ml absolute ether initiated crystallization, yielding 2.5 g hydrochloride.

Example 6

S-(2-mercaptoethyl)-6-thio-α-D-methyl-mannopyranoside

6 g of the sugar tosylate (Example 4) were dissolved in 250 ml of absolute methanol containing 20 ml of a freshly prepared solution of sodium methoxide. To the mixture was added 5 ml of 1.2 ethanedithiol. The mixture was autoclaved at 120°C for 10 hour and the reactions product was treated as above. Yield 3.1 g.

Example 7

2,3,4,6, Tetraacetyl- α -D-mannopyranosyl chloride

This compound was prepared analogously to a published procedure (D. Horton, Organic Synthesis Vol 46 p. 1, Wiley N.Y. 1966). 25 g of dried mannose were added slowly with stirring to 60 ml of acetyl chloride. The vessel was connected to a reflux condenser and the mixture was stirred for 16 hours at room temperature. Chloroform, 300 ml, was added through the condenser and the mixture was poured with vigorous stirring onto 300 g of ice and 100 ml of water. The mixture was transferred to a separatory funnel, and the organic phase was poured as fast as possible into a beaker containing ice and 300 ml of saturated sodium bicarbonate solution. The organic phase was separated and dried with 25 g of anhydrous

magnesium sulfate. The drying agent was removed, washed with dry alcohol free chloroform and the combined chloroform solution was concentrated to 35 ml at a reduced pressure in a rotatory evaporator. At 50°C ether was added to the solution until slightly turbid and the solution left at room temperature. The crystals were removed by filtration and washed with dry ether. Yield 39 g.

Example 8

S-(2-mercaptoethyl)-1-β-D-mannopyranosyl sulfide and S-(2-aminoethyl)-1-β-D-mannopyranosylsulfide

To a solution of 10 g acetochloromannose (Example 7) in 60 ml anhydrous DMF, 4 ml of 1.2 ethanedithiol or 5 g cysteamine hydrochloride and 5 of fine powdered sodium carbonate were added to the suspension which was stirred under argon for 6 hours at 70°C. The carbonate was removed and the liquid was evaporated under reduced pressure at 45°C. The residue was dissolved in absolute methanol and freshly prepared 0.1 M sodium methoxide was added to bring the pH to 8.0 and the mixture was stirred for 5 hours at room temperature. 2 ml of glacial acetic acid were added and the liquid was removed under reduced pressure. The residue was recrystallized from acetic acid. Yield 3.1 g.

Example 9

Activation of DNA with 1,2 dibromopropanal

A solution of acrolein (1.7 g) in ether was cooled on an ice bath and 1.3 ml of bromine were slowly added under stirring while waiting for the color to disappear for the next bromine addition. The ether was partially removed by blowing argon over the solution, resulting in a 2 M solution of the 1,2-dibromopropanal (Example 8). The DNA used for the following operations was in the triethylammonium form to facilitate solution in DMF.

0.5 mg of 3H fd-DNA (linear) (partly tritiated) in 250 µl of water were mixed with 3.0 ml of 0.5 M triethylammonium acetate, pH 4.5 in 70% ethanol and 50 µl of the dibromopropanal solution was added. The mixture was stirred in the dark at 37°C for 40 hours. The reaction was monitored by the appearance of fluorescence. The reaction mixture was evaporated to dryness under reduced pressure, and the DNA dissolved in 0.6 ml water and desalted by G 50 filtration with water as the eluant. The fractions containing radioactivity were combined and the volume was reduced to 0.2 ml.

Example 10

Labelling of the 3,4,5-trichloroaniline DNA with DCTA-SH

0.5 mg of the activated DNA (Example 1) in 0.2 ml of water were mixed with 2.0 ml of 0.5 M triethylammonium acetate in 90% DMF and 50 mg of DCTA-SH in the triethylammonium form were added. The mixture was stirred in the dark for 4 hours at 50°C. The DMF was removed under reduced pressure at 45°C and the DNA was desalted by G-50 filtration. The degree of labeling was then determined by the use of radioactive Ni63. On the average every 5.3 bases were labelled, by calculation.

Similar procedures were used for the biotination and glycosylation of the activated DNA using the thio derivatives of these substances (Examples 2, 6 and 8).

Chemical labelling of DNA

Rationale

Guanosine couples with certain diazonium salts at the 8 position to give stable colored products (H. Fischer, Z. Physiol. Chem. 60, 696-78, (1909)), and at position 2 to form yellow products which are acid labile (H. Kossel, Z. Physiol. Chem. 340, 210, 1965, E.N. Moudrianakis et al, Biochim. Biophys. Acta 123, 421 (1966)). The guanosine residues in the single stranded nucleic acids can couple with diazonium salts and this reaction has been used to fix single stranded

nucleic acids to cellulose (J.C. Alwine et al. Methods in Enzymology Vol. 68. p. 220-242, 1979)). If the coupled diazonium compound contains an active group that can be easily substituted by thiols or amines, then this constitutes an easy method to attach biotin or other groups to single stranded nucleic acids. 3,4,5-trichlorophenyl diazonium chloride is such a substance which has been used by the inventors to add biotin, 1,2-diaminocyclohexane-N,N,N,N-tetraacetic acid (DCTA), and some sugars to a single stranded DNA.

Another possibility to label single stranded nucleic acids is based on the fact that chloracetaldehyde reacts with adenine at pH 4.5 to form a fluorescent etheno derivative (under mild conditions). J.R. Barrio, et al Biochem. Biophys. Res. Commun. 46, 597-604, 1972), cytidine reacts at pH 3.5 and guanine at pH 6.5. At pH 4.5 guanidine does not react at all (P.D. Sattsangi, et al, J. Org. Chem., 42, 3292-3296, (1977).)

By using 1,2 dibromopropanal in place of chloracetaldehyde it was possible to derivatize DNA with an active primary bromide group, which, under mild reaction conditions, reacts with thiol or amine derivatives, offering another method of labeling DNA. These two methods are base specific.

Example 11

Terminal addition of 5'-uridine monophosphate (UMP) to linear 3H fd-DNA with Terminal Transferase and 5'-uridine triphosphate.

The incubation mixture of 600 µl contained: 400 µg of DNA, 1mM $CoCl_2$, 0.2 mM dithiothreitol, 0.1 M cacodylic acid, 25 mM tris base, 1 mM UTP and 400 units of terminal transferase. The final pH of the mixture was 6.9-7.0.

The mixture was incubated for 2 hours at 35°C. The DNA was precipitated with ethanol and dissolved in 400 µl 0.2 M sodium acetate pH 4.7.

Example 12

Oxidation of the Terminal Ribo Group and Reductive Amination. Synthesis of Amino, carboxy and thio-end substituted DNA.

The incubation mixture of 450 µl contained: 400 µg terminal labeled DNA (Example 11), 0.2 M sodium acetate pH 4.7 and 0.1 M $NaIO_4$. It was incubated for two hours at room temperature in the dark and the mixture was passed through a G 50 column equilibrated in 0.3 M potassium borate pH 9.0-9.3, fractions of 0.2 ml were collected. All radioactive fractions were combined in a total volume 1.2 ml. The DNA solution was made 0.4 M with one of the amino components (ε-aminocaproic acid, cysteamine, or 1,6-diaminohexane, using a stock solution of 1 M which

was adjusted to pH 9.3), and was incubated in the dark for 90 minutes at room temperature.

The resulting Schiff base was reduced with $NaBH_4$ as follows: $NaBH_4$ freshly dissolved to 0.2 M in water (1 ml) to M was added in four portions over 30 minute intervals. The incubation was continued for a total of 3 hours. The salts and the excess of the amino component were removed by G 50 filtration in a column equilibrated in 0.4 M sodium acetate containing 1mM beta-mercaptoethanol, the DNA-containing fractions were then combined and stored over argon at -70°C. Before use, DNA was precipitated with ethanol and dissolved in the desired buffer.

Example 13

Activation of bromoacetic acid N-hydroxysuccinimide ester

The NHS (N-hydroxy succinimide) ester of bromoacetic acid was prepared as follows: 100 mmoles of (13.9 g) of bromoacetic acid were dissolved in 50 ml of anhydrous DMF, to this solution 100 mmoles (20.6 g) of N-N-Dicyclohexylcarbodiimide were added with stirring followed by 100 mmoles of N-hydroxysuccinimide (11.9 g adjusted for 100% purity), and the mixture was stirred for 6 hours at 37°C. The mixture was then placed for 2 hours at -20°C to accelerate the precipitation of hydroxyurea, which was removed by

filtration. In the filtrate the DMF was removed under reduced pressure at 45°C and the active ester was recrystallized from 2-propanal.

Example 14

Bromoacetylation of IgG

IgG (20 mg/ml) in 0.3M potassium borate buffer pH 9.9 was mixed with 0.06 vol of a 10 mg/ml solution of the NHS ester of bromoacetic acid (Example 13) in DMSO, and the mixture was gently mixed for 1 hour at room temperature. The sample was then dialyzed against 0.1 M NaCl 0.1M phosphate buffer pH 7.5.

Example 15

Synthesis of DNA-IgG Conjugates

1.6 mg/ml of bromoacetylated IgG (Example 14) in 0.3 M potassium borate buffer were incubated at room temperature under argon with a thio-substituted, end labeled DNA solution (Example 12) of 3 mg/ml for 2 hours. Mercaptoethanol 0.01 M was then added and the mixture was further incubated at the same temperature for 2 hours to quench the unreacted bromine residues. The solution was then adsorbed on a Protein A column, and the unconjugated DNA was eluted with 1.0 M NaCl. The DNA-IgG conjugate and the unreacted IgG were eluted with isothiocyanate, and dialyzed against 0.1M

phosphate buffer, pH 7.2 to remove isothiocyanate. The conjugated IgG and the free IgG were then precipitated with ammonium sulfate 50%, the pellet dissolved in 1.0 ml phosphate buffer and the free IgG was separated from the conjugated IgG by fractionation on a Bio-Gel p-300 column equilibrated in .01M NaCl, 0.1M phosphate pH 7.2.

Example 16

Mercuration of pBR322

pBR322 DNA (100 µg) dissolved in 1 ml of 5mM sodium acetate pH 7.5 containing mercuric acetate (3 mg, .01 mmol) was reacted for 4 hours at 50°C according to a procedure of Dale et al (Nucl. Acid Res. 2:915, 1975). The 5-cytosine mercurated DNA was exhaustively dialyzed in 0.01 M Tris HCl, pH 7.5, containing 0.02 sodium chloride 2mM EDTA.

Example 17

Iodination of Mercurated pBR 322 DNA

To the mercurated DNA from the previous experiment in 1 ml 0.1M Tris HCl pH 7.5 was added 1 mg iodine using the procedure of Dale et al (Nucl. Acid Res. 2, 915, 1975). After reaction at 20°C for 2 hours the excess I_2 was extracted with chloroform and the iodinated DNA was dialyzed against 0.01m Tris HCl pH

7.5 containing 0.02M sodium chloride and 2mM EDTA. The substituted DNA was analyzed by successive digestion with N. crassa endonuclease, snake venon phosphodiesterase DNAse, and E. coli alkaline phosphatase (H. Yamasaki et al, Cancer Res. 37:1389, 1977). The mixture was eluted through DE-52 amino cellulose, and the nucleotides were analyzed by reverse phase HPLC using authentic 5-iodo-2'-deoxyuridine as a standard.

Example 18

Reaction of 5-Iodocytosine pBR322 DNA with amines. Example of reaction with 1,6-Diaminohexane.

To the iodinated DNA from the previous reaction dialyzed into 1 ml 0.1 M sodium borate was added 116 mg (1 mmol) diaminohexane. The reaction mixture was flushed with argon and heated at 100° for 2 hours. The aminohexyl substituted DNA is exhaustively dialyzed into 0.01 M Tris HCl pH 7.5.

Reaction conditions for aminocaproic acid, bis (2-aminoethane) disulfide and 6-amino-α-methyl-D-manno (Example 5) are essentially identical.

Example 19

Coupling of Amino and Carboxy-Substituted Nucleic Acids to Proteins or Amines using 1-Ethyl-3-diisopropyl-aminocarbodiimide (EDAC). Example of Streptavidin Coupled DNA

To a solution containing amino-or-carboxy-end substituted DNA (Example 11) (50 µg) and 3H-labelled Streptavidin (50 µg) dissolved in 1 ml 0.01M NaCl pH 7.5 (HCl) was added 5 mg EDAC. The reaction was incubated 20 hours in the dark and DNA was precipitated by addition of 4 M $CaCl_2$ (0.03 ml). DNA was redissolved in 1 ml water and this procedure was repeated 2 more times to remove unbound protein. The protein-coupled DNA was affinity purified in an iminobiotin-sepharose affinity column (K. Hoffman et al, PNAS 77:4666 1980) and dialyzed against 10mM NaCl.

Example 20

N-Hydroxy Succinimide Activation of Carboxyhexyl-Substituted DNA and Coupling to Proteins or Amines. Examples of Streptavidin Coupled DNA

Carboxy end substituted DNA (Example 19) (50 µg) was converted to the triethylamonium salt by shaking an aqueous solution with Dowex 50-WX (Et_3N+). The solution was lyophylized and the dried DNA was dissolved in anhydrous dimethyl formamide (0.5 ml) to which was added dicyclohexylcarbodiimide (10.3 mg, 0.05 mol) and N-Hydroxysuccinimide (5.8 mg 0.05 Mol). After incubating at room temperature for 20 hours the

reaction was centrifugated and the supernatant dialyzed for 2 hours into 10 mM NaCl. Streptavidin (50 µg) dissolved in 0.2 M borate, pH 8.5 (1 ml) was added to the N-hydroxysuccinimide activated DNA and the reaction was incubated 20 hours and dialyzed into 0.01M NaCl. The Streptaviden coupled DNA was purified by $CaCl_2$ precipitation and iminobiotin affinity chromatography as previously described.

Example 21

Reaction of DNA with Glyoxal

DNA (1 µg) (DAM insert from plasmid pDK14) was dissolved in 0.025 M glyoxal (0.2 ml) and heated at 100°C for 30 minutes in a sealed tube. The reaction was dialyzed against 10 mM NaCl. In order to assess degree of reaction on guanosine, a portion of the reaction was subjected to acid depurination by lowering the pH to 1.0 with HCl, and heating at 100°C for 30 minutes. The depurinated DNA was removed by elution through DE-52 amino cellulose and the eluted purines analyzed by HPLC on reverse phase. Comparison of peak heights of adenosine, guanosine and glyoxal-guanosine adduct (R. Shapiro et al, Biochem 5:2799, 1966) revealed that 70% of the guanosines had been substituted.

Example 22

N-biotinyl-4-amino-acetophenone

To a solution of biotin-N-hydroxysuccinimide ester (50 µg, 0.014 mmol) dissolved in 20 ml dimethylformamide (DMF) was added 4-aminophenylacetophenone (4.35 g, .03 mol) dissolved in 50 ml DMF and 100 ml 0.1 N borate buffer pH 8.5. After reaction at room temperature for 20 hours, the solvent was removed by rotary evaporation. The residual oil was triturated first with 0.1 N HCl and then with 5% sodium bicarbonate. The product was crystallized from ethanol.

Example 23

Biotinyl (4-aminophenyl)glyoxal

Selenium dioxide (0.75 g, 7 mmol) was dissolved in 4 ml dioxane containing 0.15 ml water. To this was added dropwise a solution of N-biotinyl-4-amino acetophenone (1.9 g, 7 mmol) dissolved in 5 ml dioxane. The reaction was refluxed for 3.5 hours after which the mixture was filtered and concentrated under vacuum. The crude product was purified by silica gel chromatography.

Example 24

1,N-Biotinyl-1,6-hexanediamine

Biotin-N-hydroxysuccinimide ester (1.0 g, 2.9 mmol) dissolved in dimethylformamide (5µm) was added to a solution of diaminohexane (1.15g, 10 mmol) in 0.1 M sodium borate (500 ml). After reacting at room temperature for 5 hours, the solution was rotary evaporated, redissolved in 10 ml water and chromatographed on Dowex 50 wx (H+). The column was washed with 50% aqueous methanol and the fraction eluted with triethylamine dissolved in 50% aqueous methanol (.3M) was collected. The evaporated residue was thoroughly triturated with ether and recrystallized from DMF/ether.

Example 25

CH_3-CO-CONH-$(CH_2)_6$-NH-Biotin

To a solution of pyruvic acid (.44 g, 5 mmol) cooled to 4°C, 20 ml anhydrous DMF was added isobutylchloroformated (0.64 g, 5 mmol) and tri-N-butylamine (1.43 g, 1.5 mmol). After 20 minutes at this temperature, an additional 1.4 g tri-N-butylamine was added and the mixture was added to a solution of 1,N-biotinyl-1,6-hexane diamine (Example 24) (.34 g, 1 mmol) dissolved in 30 ml DMF and 30 ml 0.1 M sodium borate. After reacting at 4°C for 1 hr. the mixture

was allowed to stand at room temperature for an additional 20 hours and subsequently concentrated in vacuo. The mixture was purified by chromatography on silica gel and the product recrystallized from ethanol.

Example 26

CHO-CO-CONH-$(CH_2)_6$-NH-Biotin

Selenium dioxide (54 mg, 0.5 mmol) was dissolved in dioxane (0.5 ml) containing 25 µl water. A solution of CH_3-CO-CONH-$(CH_2)_6$-NH-Biotin (Example 25) (0.21 g 0.5 mmol) dissolved in 1 ml dioxane was added dropwise and the reaction was heated at 100° for 4 hours. The resultant precipitate was removed by centrifugation, washed with dioxane and the supernatant was concentrated in vacuo. The crude mixture was chromatographed on silica gel.

Example 27

Reaction of DNA with Biotinylated Glyoxal Derivatives

DNA (1 µg) as a triethylammonium salt was dissolved in 100 µl water. To this was added 100 µl of a solution of (N-biotinyl (4-aminophenyl)) glyoxal (0.05 M) or CHO-CO-CONH-$(CH_2)_6$-NH-Biotin (0.05H) in dimethylformamide. The mixture was heated at 100°C for 30 minutes in a sealed tube and subsequently dialyzed against 0.01 M NaCl. Extent of

reaction was determined by acid depurification and HPLC assay of purine nucleosides, as described previously.

Example 28

Bromination of pBR 322 DNA

To a solution of pBR 322 DNA (100 µg) dissolved in 0.5 M acetate buffer pH 5.5. was added bromine (5.5 µl, 0.1 mmol). The reaction was incubated at 60° for 30 hours and exhaustively dialyzed against 0.01 M NaCl.

Example 29

Reaction of Brominated pBR 322 DNA with Thiols. Example of Reaction with Cysteamine and 3-Mercaptopropionic acid.

A solution of brominated pBR 322 DNA (500 µg) in 0.1 M borate pH 8.5 (1 ml) was incubated with either cysteamine or 3-mercaptopropionic acid (20 mg) for 20 hours at room temperature under an argon atmosphere. The resultant amine-or carboxy- substituted DNA was dialyzed against 0.01 M NaCl.

Example 30

Reaction of Brominated pBR322 DNA with Amines. Example of Reaction with 1,6-Diaminohexane

A solution of brominated pBR 322 DNA (100 µg) and 1 M of 1,6-diaminohexane (1ml) were heated at 65° for 3 hours under an argon atmosphere. The resultant amine-sbustituted DNA was dialyzed against 0.1 M NaCl.

Example 31

Synthesis of a Protein Coupled to a Signal Generating Polynucleotide. Example of IgG Coupled to Chemically Radio-labeled DNA.

Pd DNA was end labelled with UMP using terminal transferase under conditions described in Example 11. The end labelled DNA was derivatized with 2,4,5-trichloroaniline (Example 1) and reacted with DCTA-SH under identical conditions to those described in Example 1a. The end labelled, DCTA derivatized DNA was oxidized with sodium periodate, reacted with cysteamine and reduced with sodium borohydride as described in Example 12. This was in turn reacted with bromoacetylated IgG (Example 14) using conditions described in Example 15.

Example 32

Use of Bacteriophage M13 as Bridging Entity

Using techniques of recombinant DNA technology, an asymmetric DNA sequence can be inserted in the replicative (double-stranded form) of a single-stranded phage such as M13. One strand of the insert will be deficient in guanine residues. As a result of this insertion, two single-stranded phages will be obtained in both polarities, one containing the (G-) strand, i.e., no guanylate residues of the asymmetric sequence,

the other containing the sequence complementary to the G(-) sequence, to be called the G(+) sequence.

The G(+) phage is used as the vector (bridging entity) for carrying a DNA probe of interest such as, for example, herpes simplex virus I DNA sequences.

The G(-) phage (signalling entity) is chemically reacted with a guanosine specific reagent, such as a 1,2-dicarbonyl reagent. The G(-) insert in the G(-) phage would not be modified because it lacks guanylate residues.

A general protocol for the preparation of single-stranded M13 would be as follows:

1. M13 mp8 rf (replicative form, double-stranded), is grown. It is cut with Hinc II, which leaves blunt ends.
2. pd(G-T)$_5$ and pd(A-C)$_5$ are provided and hybridized to form a perfect double-strand. The ends must be perfectly matched. In order to obtain this condition it is necessary to use high C_0t conditions for hybridization.
3. The hybrids are ligated in the presence of the restriction enzyme Rsa I. Rsa I recognizes the sequence GTAC, and hence will cut to leave blunt ends and proofread the ligation.
4. The ligation products are isolated. They are double-stranded poly d (G-T) poly d (A-C).

(Any complementary, repeating, low complexity sequence can be used. The subsequent modification and chemistries must be adjusted accordingly.)

5. Alkaline phosphatase is used to remove 5' phosphates.
6. Polynucleotide kinase and ^{32}P-ATP are used to replace 5' ends with ^{32}P-phosphates.
7. The reaction mixture is run over 15-20% non-denaturing polyacrylamide gels to separate the different size fragments.
8. The fragments are located on gels by autoradiography.
9. The desired size bands are eluted out of the gel by cutting, mashing and then extracting the gel with high salt buffer. Fragments having 50-100 bp or larger are preferred.
10. DNA is concentrated by any of a number of possible techniques, such as ethanol precipitation, spermine precipitation, lyophilization, or the like.
11. The fragments are ready to be cloned into Hinc II-cut M13.

Using a standard cloning technique, the following sequence is performed:

a. Fragments are ligated into M13;

b. Cells (for example E. coli JM103) are transformed with the M13;

c. Transformed cells are plated; and

d. Recombinants are selected.

12. There are two possible routes for selection of recombinants:

a. If a known size class has been inserted, plaques will be picked and sequenced to check for the presence of insert.

b. An alternative procedure is to shotgun all the sequences made in step 4 into M13. This protocol requires that many more clones be picked and then checked by sequencing.

13. Once a suitable clone has been obtained (M13 with the appropriate size sequence), the strand that gives GTGT, etc., in the single-strand replicating form will be selected. This clone is then used for further genetic engineering by inserting sequences from a variety of pathogens into the replicating form.

14. The strand that gives ACAC etc. in the replicating form is cloned in mass culture and chemically modified with a reporter (signal generation portion) that is specific for G's. Thus the G(-) phage is exhaustively reacted with the bifunctional reagent p-azidophenyl glyoxal (APG). The dicarbonyl moiety of APG reacts only with guanosine residues in single-stranded portions of the DNA. The insert lacking guanosine is not affected by this treatment.

15. The (G+) and derivatized (G-) DNAs are mixed in equimolar concentration and allowed to hybridize to target DNAs and to each other. Visualization of the hybrids is by standard signal reporting techniques.

Having now fully described this invention, it will be understood by those of ordinary skill in the art that the same can be subject to a wide range of modifications, to generate equivalent systems and processes, without affecting the spirit or scope of the invention or of any embodiment described therein.

WHAT IS CLAIMED AS NEW AND INTENDED TO BE COVERED BY LETTERS PATENT OF THE UNITED STATES IS:

1. A method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises:

Providing a molecular bridging entity (B) having thereon:

(i) a portion capable of recognizing said molecularly recognizable portion on said analyte; and

(ii) a portion comprising a polynucleotide sequence; and

(C) a signalling entity having thereon:

(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity, thereby to form a stable polynucleotide hybrid, and

(ii) a signal generating portion;

forming a complex comprising:

(1) said analyte (A) complexed through said molecularly recognizable portion to

(2) said recognizing portion of said entity (B); said entity (B) being

complexed through said polynucleotide portion thereon to

(3) said polynucleotide portion of said signalling entity (C); and

detecting a signal by means of said signal generating portion present in said complex.

2. The method of Claim 1 wherein said analyte is present in a biological or non-biological sample.

3. The method of Claim 1 wherein said molecularly recognizable portion on said analyte is proteinaceous.

4. The method of Claim 1 wherein the molecularly recognizable portion on said analyte comprises nucleic acid.

5. The method of Claim 1 wherein the molecularly recognizable portion on said analyte comprises a saccharide.

6. The method of any of Claims 3, 4 or 5 wherein said analyte is selected from the group consisting of an antigen, an antibody, a receptor, a virus, a viral component, a bacterium, a bacterial component, a cell, a cellular component, or any pathogenic or non-pathogenic component of a sample.

7. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises a polynucleotide sequence.

8. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises an antigen.

9. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises an antibody.

10. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises a saccharide.

11. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises a lectin.

12. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises a hormone.

13. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises a receptor.

14. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises an enzyme inhibitor or enzyme cofactor.

15. The method of Claim 1 wherein said recognizing portion on said bridging entity comprises an enzyme active site, a cofactor binding site, or a receptor protein.

16. The method of Claim 1 wherein said polynucleotide sequence on said bridging entity codes for a gene product or fragment thereof.

17. The method of Claim 1 wherein said polynucleotide sequence on said bridging entity does not code for a gene sequence or fragment thereof.

18. The method of Claim 1 wherein said polynucleotide sequence on said bridging entity comprises a poly deoxy G, poly deoxy C, poly deoxy T or poly deoxy A sequence, or any poly-ribo or -deoxyribo purine, pyrimidine or analog.

19. The method of Claim 1 wherein said polynucleotide sequence on said bridging entity comprises a sequence portion which is rich in guanosine residues.

20. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to another polynucleotide sequence.

21. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antibody.

22. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antigen.

23. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a saccharide.

24. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a lectin.

25. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a hormone.

26. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to a receptor.

27. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme inhibitor or enzyme cofactor.

28. The method of Claim 1 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme.

29. The method of Claim 7 wherein said bridging entity is a circular DNA polymer.

30. The method of Claim 29 wherein said DNA is single-stranded.

31. The method of Claim 29 wherein said circular DNA polymer is derived from a filamentous phage.

32. The method of Claim 31 wherein said filamentous phage is M13 or a variant thereof.

33. The method of Claim 32 wherein said M13 phage carries a sequence portion which is rich in guanosine residues, or cytosine residues.

34. The method of Claim 1 wherein said polynucleotide portion on said signalling entity codes for a gene product or fragment thereof.

35. The method of Claim 1 wherein said polynucleotide portion on said signalling entity does not code for a gene product or fragment thereof.

36. The method of Claim 1 wherein said polynucleotide portion on said signalling entity comprises a poly deoxy C, poly deoxy G, poly deoxy A, poly deoxy T sequence, or a repeating sequence of low complexity.

37. The method of Claim 1 wherein said polynucleotide portion on said signalling entity comprises a sequence portion which is rich in cytosine residues, or guanosine residues.

38. The method of Claim 1 wherein said signalling entity is a polynucleotide polymer.

39. The method of Claim 38 wherein said polynucleotide polymer is a naturally occurring modified DNA.

40. The method Claim 39, wherein said polynucleotide polymer is derived from a T (even) phage.

41. The method of Claim 40 wherein said T (even) phage phage is T_4.

42. The method of Claim 39 wherein said modified DNA carries a cloned insert.

43. The method of Claim 38 wherein said polymer is single-stranded.

44. The method of Claim 43, wherein said polymer is derived from a filamentous phage.

45. The method of Claim 44 wherein said phage is M13 or a variant thereof.

46. The method of Claim 1 wherein said signal generating portion of said signalling entity is radiolabeled.

47. The method of Claim 1 wherein said signal generating portion of said signalling entity is not radiolabeled.

48. The method of Claim 47 wherein said signal generating portion comprises an enzyme.

49. The method of Claim 47 wherein said signal generating portion comprises a biotin moiety.

50. The method of Claim 47 wherein said signal generating portion comprises a fluorogenic compound.

51. The method of Claim 47 wherein said signal generating portion comprises an electron dense compound.

52. The method of Claim 47 wherein said signal generating portion comprises or binds to an insoluble phase.

53. The method of Claim 52 wherein said insoluble phase comprises a latex particle, a resin, or a bacterium.

54. The method of Claim 47 wherein said signal generation portion comprises an antibody or antigen.

55. The method of Claim 47 wherein said signal generating portion comprises a saccharide or lectin.

56. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises a radioactivity measurement.

57. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises an enzymatic reaction.

58. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises a fluorescence measurement, or electron microscopic measurement.

59. The method of Claim 47 wherein said signal generating portion is a polynucleotide sequence capable of recognizing a signal containing moiety.

60. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises an antibody/antigen complexation reaction.

61. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises a complexation reaction between biotin and a biotin binding moiety.

62. The method of Claim 61 wherein said moiety is avidin, streptavidin or an anti-biotin antibody.

63. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises detection of an electron dense compound.

64. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises a complexation reaction between a saccharide and a lectin.

65. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises a binding step on an insoluble phase.

66. The method of Claim 1 wherein said step of detecting a signal by means of said signal generating portion comprises complexation between a signalling entity comprising a cloned insert on a naturally occurring modified DNA, and the bridging moiety, followed by binding a modified lectin to said signalling entity.

67. The mthod of Claim 66 wherein said modified DNA is derived from a T_4 phage.

68. The method of Claim 65 wherein said insoluble phase is a latex particle.

69. The method of Claim 1 wherein said recognizable portion on said analyte is a

polynucleotide sequence, said recognizing portion on said bridging entity is a polynucleotide sequence capable of stably annealing thereto, said bridging entity is a single-stranded DNA polymer, and said step of detection by means of said signal generating portion on said signalling entity is based on non-radioactive detection.

70. The method of Claim 69 wherein said bridging entity is derived from a filamentous phage.

71. The method of Claim 69 wherein said signalling entity is derived from a filamentous phage.

72. A polynucleotide sequence covalently attached to an antibody.

73. The sequence of Claim 72 wherein said antibody is monoclonal.

74. A polynucleotide sequence covalently attached to a lectin.

75. A polynucleotide sequence covalently attached to a saccharide having up to 20 saccharide units.

76. A polynucleotide sequence covalently attached to receptor.

77. A polynucleotide sequence covalently attached to a hormone.

78. A DNA molecule carrying a polynucleotide portion which comprises a sequence selected from the group consisting of poly dGT, poly dAC, poly dCT, poly

dAt, poly dGC, poly dGA, poly dG, poly dC, poly dT, poly dA, and a repeating low-complexity polynucleotide.

79. The DNA molecule of Claim 78 which is a filamentous phage.

80. The phage of Claim 79 which is M13 or a variant thereof.

81. The DNA molecule of any of Claims 78 or 79 wherein said sequence is at least an oligonucleotide.

82. The DNA molecule of any of Claims 78 or 79 which also carries a polynucleotide sequence complementary to part of whole of a gene sequence of a nucleic acid-containing organism.

83. The DNA molecule of Claim 82 wherein said organism is a virus, a prokaryotic or a eukaryotic cell.

84. The DNA molecule of Claim 83 wherein said prokaryotic cell is a bacterium.

85. The DNA molecule of Claim 83 wherein said eukaryotic cell is a mammalian cell.

86. The DNA molecule of Claim 82 which is a filamentous phage.

87. The DNA molecule of Claim 82 which is M13 or a variant thereof.

88. A circular DNA molecule covalently attached to a non radiolabelled signal generating moiety.

89. The DNA molecule of Claim 88 which is a filamentous phage.

90. The DNA molecule of any of Claims 88 or 89 which carries a polynucleotide portion which comprises a sequence selected from the group consisting of poly dGT, poly dAC, poly dCT, poly dAT, poly dGC, poly dGA, poly dG, poly dC, poly dT, poly dA and a repeating low-complexity polynucleotide.

91. The DNA molecule of any of Claims 88 or 89 which carries a polynucleotide portion which is rich in cytosine residues.

92. The DNA molecule of Claim 90 wherein said sequence is an oligonucleotide.

93. The DNA molecule of any of Claims 88 or 89 which carries a polynucleotide portion which comprises a sequence coding for part or whole of a gene.

94. The DNA molecule of any of Claims 88 or 89 wherein said signal generating moiety comprises a radiolabel.

95. The DNA molecule of any of Claims 88 or 89 wherein said signal generating moiety is non-radiolabeled.

96. The DNA molecule of Claim 93 wherein said signal generating moeity comprises an enzyme.

97. The DNA molecule of Claim 93 wherein said signal generating moiety comprises a biotin moiety.

98. The DNA molecule of Claim 93 wherein said signal generating moeity comprises an antibody.

99. The DNA molecule of Claim 93 wherein said signal generating moeity comprises a fluorogenic compound.

100. A kit useful for the detection of an analyte (A) having a molecularly recognizable portion thereon, comprising:

I) a carrier being compartmentalized to receive in close confinement therein one or more container means;

II) a first container means containing a molecular bridging entity (B) having thereon:

(i) a portion capable of recognizing said molecularly recognizble portion on said analyte (A); and

(ii) a portion comprising a polynucleotide sequence; and

(III) a second container means containing a signalling entity (C) having thereon:

(i) a polynucleotide portion capable of annealing to said polynucleotide portion of said bridging entity (B) thereby to

form a stable polynucleotide hybrid; and

~~(ii) a signal-generating portion.~~

~~101. The kit of Claim 100 which also comprises~~ cancelled per B

IV) a third container means containing components needed to detect a signal from said signal generating means.

102. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises a polynucleotide sequence.

103. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises an antigen.

104. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises an antibody.

105. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises a saccharide.

106. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises a lectin.

107. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises a hormone.

108. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises a receptor.

109. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises an anzyme inhibitor or enzyme cofactor.

110. The kit of Claim 100 wherein said recognizing portion on said bridging entity comprises an enzyme active site or cofactor binding site.

111. The kit of Claim 100 wherein wherein said polynucleotide sequence on said bridging entity codes for a gene product or fragment thereof.

112. The kit of Claim 100 wherein said polynucleotide sequence on said bridging entity does not code for a gene product or fragment thereof.

113. The kit of Claim 100 wherein said polynucleotide sequence on said bridging entity comprises a poly dG, poly dC, poly dT, poly dA sequence, or a low complexity (repeating) polynucleotide.

114. The kit of Claim 100 wherein said polynucleotide sequence on said bridging entity comprises a sequence portion which is rich in guanosine residues.

115. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to another polynucleotide sequence.

116. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antibody.

117. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to an antigen.

118. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a saccharide.

119. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a lectin.

120. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a hormone.

121. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to a receptor.

122. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme inhibitor or enzyme cofactor.

123. The kit of Claim 100 wherein said polynucleotide sequence in said bridging entity is covalently attached to an enzyme.

124. The kit of Claim 100 wherein said bridging entity is a circular DNA polymer.

125. The kit of Claim 124 wherein said circular DNA is single-stranded.

126. The kit of Claim 125 wherein said circular DNA polymer is derived from a filamentous phage.

127. The kit of Claim 124 wherein said filamentous phage is M13 or a variant thereof.

128. The kit of Claim 125 wherein said M13 phage carries a sequence portion which is rich in guanosine or cytosine residues.

129. The kit of Claim 100 wherein said polynucleotide portion on said signalling entity codes for a gene product or fragment thereof.

130. The kit of Claim 100 wherein said polynucleotide portion on said signalling entity does not code for a gene product or fragment thereof.

131. The kit of Claim 100 wherein said polynucleotide portion on said signalling entity comprises a poly dC, poly dG, poly dA, poly dT sequence, or a low-complexity, repeating polynucleotide.

132. The kit of Claim 100 wherein said polynucleotide portion on said signalling entity comprises a sequence portion which is rich in cytosinee or guanosine residues.

133. The kit of Claim 100 wherein said signalling entity is a circular DNA polymer.

134. The kit of Claim 133 wherein said DNA is single-stranded.

135. The kit of Claim 134 wherein said DNA is derived from a filamentous phage.

136. The kit of Claim 135 wherein said phage is M13 or a variant thereof.

137. The kit of Claim 100 wherein said signal generating portion on said signalling entity is radiolabeled.

138. The kit of Claim 100 wherein said signal generating portion of said signalling entity is not radiolabeled.

139. The kit of Claim 138 wherein said signal generating portion comprises an enzyme.

140. The kit of Claim 138 wherein said signal generating portion comprises a biotin moiety.

141. The kit of Claim 138 wherein said signal generating portion comprises a fluorogen.

142. The kit of Claim 138 wherein said signal generating portion comprises an electron dense compound.

143. The kit of Claim 138 wherein said signal generating portion comprises or binds to an insoluble phase.

144. The kit of Claim 138 wherein said insoluble phase comprises a latex particle, a resin, or a bacterium.

145. The kit of Claim 138 wherein said signal generating portion comprises an antibody.

146. The kit of Claim 138 wherein said signal generating portion comprises a saccharide.

147. The kit of Claim 100 wherein said recognizable portion on said analyte is a polynucleotide sequence, said recognizing portion on said bridging entity is a polynucleotide sequence capable of stably annealing thereto, said bridging entity is a single-stranded DNA polymer, and said signal generating portion on said signalling entity is based on non-radioactive detection.

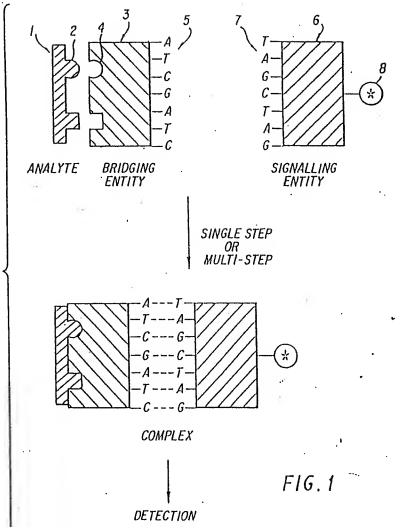
148. The kit of Claim 147 wherein said bridging entity is derived from a filamentous phage.

149. The kit of Claim 147 wherein said signalling entity is derived from a filamentous phage.

ABSTRACT OF THE DISCLOSURE

A method of detecting in a sample an analyte (A) having a molecularly recognizable portion thereon, which comprises: providing (B) a molecular bridging entity having thereon: (i) a portion capable of recognizing the molecularly recognizable portion on the analyte; and (ii) a portion comprising a polynucleotide sequence; and (C) a signalling entity having thereon: (i) a polynucleotide portion capable of annealing to the polynucleotide portion of the bridging entity, thereby to form a stable polynucleotide hybrid, and (ii) a signal generating portion; forming a complex comprising: (1) the analyte (A) complexed through its molecularly recognizable portion to (2) the recognizing portion of the entity (B); the entity (B) being complexed through the polynucleotide portion thereon to (3) the polynucleotide portion of the signalling entity; and detecting a signal by means of the signal generating portion present in the complex.

192/kdg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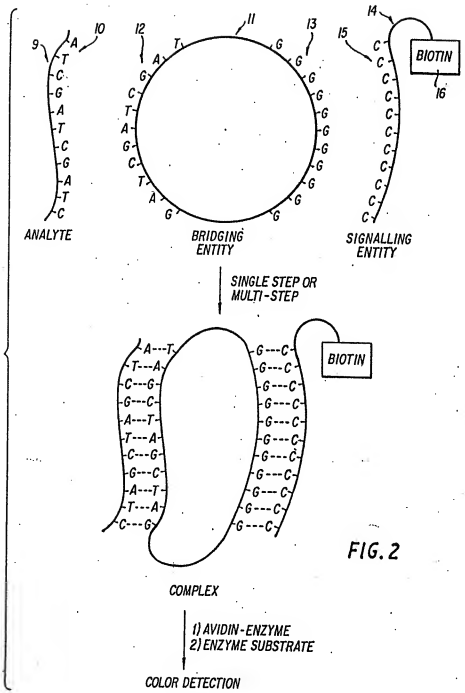
2
4
3
5
A
T
C
G
A
T
C
7
6
T
A
G
C
T
A
G
8
ANALYTE
BRIDGING ENTITY
SIGNALLING ENTITY
SINGLE STEP OR MULTI-STEP
A---T
T---A
C---G
G---C
A---T
T---A
C---G
COMPLEX
DETECTION

FIG. 1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T
C
ANALYTE
12
11
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G
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C
T
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C
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BRIDGING ENTITY
14
15
BIOTIN
16
C
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C
C
C
C
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C
C
C
C
SIGNALLING ENTITY
SINGLE STEP OR MULTI-STEP
BIOTIN
A---T
T---A
C---G
G---C
A---T
T---A
C---G
G---C
A---T
T---A
C---G
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
G---C
COMPLEX
1) AVIDIN-ENZYME
2) ENZYME SUBSTRATE
COLOR DETECTION

FIG. 2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s):	Pergolizzi et al.	
Serial No.:	08/479,995	Group Art Unit: 1631
Filed:	June 7, 1995	Primary Exam'r: John S. Brusca
For:	**ANALYTE DETECTION UTILIZING POLYNUCLEOTIDE SEQUENCES, COMPOSITION, PROCESS AND KIT** (As Previously Amended)	

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LISTING OF CLAIMS ACCOMPANYING REQUEST FOR VOLUNTARY PUBLICATION OF PATENT APPLICATION UNDER 37 C.F.R. §1.221(a)

Dear Sirs:

The following listing of claims and remarks are submitted concurrently with a request for voluntary publication under 37 C.F.R. §1.221(a), in the above-identified application.

A Listing of Claims begin on page 2 of this paper; and

Remarks begin on page 60 of this paper.

LISTING OF CLAIMS

The following is a listing of claims in this application.

CLAIMS 1-282. (Canceled)

CLAIM 283. (Previously Presented) A composition of matter comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 284. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion or portions on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 285. (Previously Presented) A composition of matter comprising:

Enz-11(C2)(D1)(C2)

a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 286. (Previously Presented) A composition of matter comprising:
a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 287. (Previously Presented) A composition of matter comprising:

a first part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of

hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 288. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 289. (Previously Presented) A composition of matter comprising a complex which comprises:

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 290. (Previously Presented) A composition of matter comprising a complex which comprises:

Enz-11(C2)(D1)(C2)

an analyte having one or more molecularly recognizable portions thereon;

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 291. (Previously Presented) A composition of matter comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal.

CLAIM 292. (Previously Presented) A composition of matter comprising a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such

entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal.

CLAIM 293. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal.

CLAIM 294. (Previously Presented) A composition of matter comprising:
a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal.

CLAIM 295. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said analyte comprises a biological system.

CLAIM 296. (Previously Presented) The composition according to claim 295, wherein said biological system comprises at least one member selected from the group consisting of a virus or a viral component thereof, and a cell or a cellular component thereof.

CLAIM 297. (Previously Presented) The composition according to claim 296, wherein said cell or component thereof comprises a bacterium or a bacterial component thereof.

CLAIM 298. (Previously Presented) The composition according to claim 295, wherein said biological system comprises a pathogen or a component thereof.

CLAIM 299. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said analyte is selected from the group consisting of a nucleic acid and a protein.

CLAIM 300. (Previously Presented) The composition according to claim 299, wherein said analyte nucleic acid is selected from the group consisting of an oligo- or polyribonucleotide, an oligo- or polydeoxyribonucleotide, a poly-purine, a poly-pyrimidine, and a nucleotide analog-containing nucleic acid polymer, or any combination of the foregoing.

CLAIM 301. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion comprises a low molecular weight organic compound.

CLAIM 302. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion is selected from the group consisting of an antigen and an antibody.

CLAIM 303. (Previously Presented) The composition according to claim 302, wherein said antibody comprises a polyclonal or a monoclonal antibody.

CLAIM 304. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion is selected from the group consisting of a saccharide and a lectin.

CLAIM 305. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion is selected from the group consisting of a hormone and a receptor therefor.

CLAIM 306. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion is selected from the group consisting of an enzyme, an allosteric effector, an enzyme substrate and an enzyme cofactor.

CLAIM 307. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion is selected from the group consisting of a ligand and a receptor therefor.

CLAIM 308. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular

bridging recognizing first portion is selected from the group consisting of a protein and a protein receptor therefor.

CLAIM 309. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging recognizing first portion comprise a nucleic acid.

CLAIM 310. (Previously Presented) The composition according to claim 309, wherein said nucleic acid comprises an oligo- or polynucleotide.

CLAIM 311. (Previously Presented) The composition according to claim 310, wherein said oligo- or polynucleotide comprises a modified oligo- or polynucleotide.

CLAIM 312. (Previously Presented) The composition according to claim 310 wherein said oligo- or polynucleotide comprises one or more nucleotides modified on the sugar phosphate, base, or combinations thereof.

CLAIM 313. (Previously Presented) The composition according to claim 310, wherein said oligo- or polynucleotide is single-stranded or partially double-stranded.

CLAIM 314. (Previously Presented) The composition according to claim 310, wherein said oligo- or polynucleotide is circular or linear.

CLAIM 315. (Previously Presented) The composition according to claim 310, wherein said oligo- or polynucleotide is selected from the group consisting of an oligo- or polyribonucleotide, an oligo- or polydeoxyribonucleotide, a poly-purine, a poly-pyrimidine and a nucleotide analog-containing oligo- or polynucleotide, or any combination of the foregoing.

CLAIM 316. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said nucleic acid sequence or segment in the molecular bridging entity second portion comprises an oligo- or polynucleotide.

CLAIM 317. (Previously Presented) The composition according to claim 315, wherein said oligo- or polynucleotide comprises a modified oligo- or polynucleotide.

CLAIM 318. (Previously Presented) The composition according to claim 316, wherein said oligo- or polynucleotide comprises one or more nucleotides modified on the sugar, phosphate, base or combinations thereof.

CLAIM 319. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said nucleic acid sequences or segments in the molecular bridging entity second portion is single-stranded or partially double-stranded.

CLAIM 320. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said nucleic acid sequences or segments in the molecular bridging entity second portion is linear or circular.

CLAIM 321. (Previously Presented) The composition according to claim 316, wherein said oligo- or polynucleotide is selected from the group consisting of an oligo- or polyribonucleotide, an oligo- or polydeoxyribonucleotide, a poly-purine, a poly-pyrimidine and a nucleotide analog-containing oligo- or polynucleotide, or any combination of the foregoing.

CLAIM 322. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said nucleic acid

sequences or segments in the molecular bridging entity second portion is derived from a phage selected from the group consisting of a T even phage, a filamentous phage, an M13 phage, or, an M13 phage variant.

CLAIM 323. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging entity second portion comprises a nucleic acid sequence or segment of repeating low complexity.

CLAIM 324. (Previously Presented) The composition according to claim 323, wherein said nucleic acid sequence or segment of repeating low complexity is selected from the group consisting of a poly G or polydeoxy G, poly GT or polydeoxy GT, poly C or polydeoxy C, poly T or polydeoxy T, poly A or polydeoxy A, poly CA or polydeoxy CA, poly GA or polydeoxy GA, poly GAT or polydeoxy GAT, and poly GTA or polydeoxy GTA.

CLAIM 325. (Previously Presented) The composition according to claim 310, wherein said molecular bridging entity first portion and said molecular bridging entity nucleic acid second portion are incapable of hybridizing to identical oligo- or polynucleotide sequences.

CLAIM 326. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said nucleic acid sequences or segments in the molecular bridging entity second portion are covalently attached to one another.

CLAIM 327. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signalling entity nucleic acid portion comprises an oligo- or polynucleotide.

Enz-11(C2)(D1)(C2)

CLAIM 328. (Previously Presented) The composition according to claim 327, wherein said signalling entity oligo- or polynucleotide is selected from the group consisting of an oligo- or polyribonucleotide, an oligo- or polydeoxyribonucleotide, a poly-purine, a poly-pyrimidine and a nucleotide analog-containing oligo- or polynucleoide, or any combination of the foregoing.

CLAIM 329. (Previously Presented) The composition according to claim 327, wherein said oligo- or polynucleotide comprises a modified oligo- or polynucleotide.

CLAIM 330. (Previously Presented) The composition according to claim 327, wherein said oligo- or polynucleotide comprises one or more nucleotides modified on the sugar, phosphate, base or combinations thereof.

CLAIM 331. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signalling entity nucleic acid portion is single-stranded or partially double-stranded.

CLAIM 332. (Previously Presented) The composition according to any of the claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signalling entity nucleic acid portion is linear or circular.

CLAIM 333. (Previously Presented) The composition according to claim 332, wherein said signalling entity nucleic acid portion is a polymer derived from a linear or circular nucleic acid molecule covalently attached to a signal generating portion or a signalling chemical moiety.

CLAIM 334. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signalling entity nucleic acid portion is derived from a phage selected from the group consisting of a T even phage, a filamentous phage, and an M 13 phage, or an M13 phage variant.

Enz-11(C2)(D1)(C2)

CLAIM 335. (Previously Presented) The composition according to claim 329, wherein said signalling entity modified oligo- or polynucleotide comprises a naturally occurring modified oligo- or polynucleotide.

CLAIM 336. (Previously Presented) The composition according to claim 335, wherein said signalling entity modified oligo- or polynucleotide carries a cloned insert.

CLAIM 337. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signalling entity nucleic acid portion comprises a nucleic acid sequence or segment of repeating low complexity.

CLAIM 338. (Previously Presented) The composition according to claim 337, wherein said nucleic acid sequence or segment of repeating low complexity is selected from the group consisting of a poly G or polydeoxy G, poly GT or polydeoxy GT, poly C or polydeoxy C, poly T or polydeoxy T, poly A or polydeoxy A, poly CA or polydeoxy CA, poly GA or polydeoxy GA, poly GAT or polydeoxy GAT, and poly GTA or polydeoxy GTA.

CLAIM 339. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signal generating portion or said one or more chemically modified or artificially altered polynucleotides are capable of directly providing a detectable signal.

CLAIM 340. (Previously Presented) The composition according to claim 339, wherein said direct signal providing signal generating portion comprises a radioactive compound.

CLAIM 341. (Previously Presented) The composition according to claim 339, wherein said direct signal providing signal generating portion is selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound and an electron dense compound.

CLAIM 342. (Previously Presented) The composition according to claim 339, wherein said direct signal providing signal generating portion comprises an enzyme.

CLAIM 343. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signal generating portion or said one or more chemically modified or artificially altered polynucleotides are indirectly capable of indirectly providing a detectable signal.

CLAIM 344. (Previously Presented) The composition according to claim 343, wherein said indirect signal providing signal generating portion is selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand and an enzyme.

CLAIM 345. (Previously Presented) The composition according to claim 343, wherein said indirect signal providing signal generating portion comprises a polynucleotide sequence capable of recognizing a signal-containing moiety.

CLAIM 346. (Previously Presented) The composition according to claim 343, wherein said indirect signal providing signal generating portion comprises a compound capable of binding to an insoluble phase.

CLAIM 347. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signal generating portion or said one or more chemically modified or artificially altered polynucleotides are capable of being detected by a member selected from the group consisting of an enzymatic measurement, a fluorescent measurement, a phosphorescent measurement,

a chemiluminescent measurement, a colorimetric measurement, a microscopic measurement, an electron density measurement, and a radioactive measurement.

CLAIM 348. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is greater than 5.

CLAIM 349. (Previously Presented) The composition according to claim 348, wherein the ratio is greater than 10.

CLAIM 350. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein the ratio of the signal generating portions or the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is greater than 1.

CLAIM 351. (Previously Presented) The composition according to claim 350, wherein the ratio is greater than 5.

CLAIM 352. (Previously Presented) The composition according to claim 351, wherein the ratio is greater than 10.

CLAIM 353. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is greater than 1, and the ratio of the signal generating portions or the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities are greater than 1.

CLAIM 354. (Previously Presented) The composition according to claim 353, wherein one or both ratios are greater than 5.

CLAIM 355. (Previously Presented) The composition according to claim 354, wherein one or both ratios are greater than 10.

CLAIM 356. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein the ratio of signalling entities to molecular bridging entity is greater than 5.

CLAIM 357. (Previously Presented) The composition according to claim 356, wherein the ratio is greater than 10.

CLAIM 358. (Previously Presented) The composition according to any of claims 284, 286, 288, 290, 293 or 294, wherein the analyte is immobilized.

CLAIM 359. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein the molecular bridging entity is immobilized.

CLAIM 360. (Previously Presented) An article of manufacture comprising:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion nucleic acid sequences or segments, and one or more signal generating portions, each capable of providing a detectable signal.

CLAIM 361. (Previously Presented) An article of manufacture comprising:

Enz-11(C2)(D1)(C2)

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion nucleic acid sequences or segments, and one or more polynucleotides which have been chemically modified or artificially altered.

CLAIM 362. (Previously Presented) The article of manufacture according to claims 360 or 361, further comprising the analyte.

CLAIM 363. (Canceled)

CLAIM 364. (Previously Presented) The process according to claims 443, 445 or 447 characterized in that said forming step comprises contacting said analyte with said bridging entity to form a first complex and thereafter contacting the first complex with said signalling entity to form said complex recited in said forming step.

CLAIM 365. (Previously Presented) The process according to claims 443, 445 or 447, characterized in that said forming step comprises contacting said bridging entity with said signalling entity under conditions sufficient to form a first complex and thereafter contacting the first complex with said analyte under conditions sufficient to form said complex recited in said forming step.

CLAIM 366-381. (Canceled)

CLAIM 382. (Previously Presented) The process according to claims 449, 451 or 453, characterized in that said forming step comprises contacting said analyte with said bridging entity to form a first complex and thereafter contacting the first complex with said signalling entity to form said complex recited in said forming step.

Enz-11(C2)(D1)(C2)

CLAIM 383. (Previously Presented) The process according to claims 449, 451 or 453, characterized in that said forming step comprises contacting said bridging entity with said signalling entity under conditions sufficient to form a first complex and thereafter contacting the first complex with said analyte to form said complex recited in said forming step.

CLAIM 384-399. (Canceled)

CLAIM 400. (Previously Presented) The process according to claims 455, 457 or 458, characterized in that said forming step comprises contacting said fixed or immobilized analyte with said bridging entity to form a first complex and thereafter contacting the first complex with said signalling entity to form said complex comprising said composition and said analyte recited in said forming step.

CLAIM 401. (Previously Presented) The process according to claims 455, 457 or 458, characterized in that said forming step comprises contacting said bridging entity with said signalling entity under conditions sufficient to form a first complex and thereafter contacting the first complex with said fixed or immobilized analyte under conditions sufficient to form said complex comprising said composition and said analyte recited in said forming step.

CLAIM 402. (Canceled)

CLAIM 403. (Previously Presented) The process according to claim 400, further comprising one or more washing steps prior to detection.

CLAIM 404. (Previously Presented) The process according to claim 401, further comprising one or more washing steps prior to detection.

CLAIM 405. (Canceled)

CLAIM 406. (Previously Presented) The process according to claim 459, characterized in that said forming step comprises contacting said fixed or immobilized analyte with said bridging entity to form a first complex and thereafter contacting the first complex with said signalling entity to form said complex comprising said composition and said analyte recited in said forming step.

CLAIM 407. (Previously Presented) The process according to claim 459 characterized in that said forming step comprises contacting said bridging entity with said signalling entity under conditions sufficient to form a first complex and thereafter contacting the fixed or immobilized analyte with the first complex under conditions sufficient to form said complex comprising said composition and said analyte recited in said forming step.

CLAIM 408. (Canceled)

CLAIM 409. (Previously Presented) The process according to claim 406, further comprising one or more washing steps prior to detection.

CLAIM 410. (Previously Presented) The process according to claim 407, further comprising one or more washing steps prior to detection.

CLAIM 411. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

(i) a container carrying a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable portion on said analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

(ii) a container carrying more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging

entity second portion nucleic acid sequence or segment, and one or more signal generating portions, each such portion being capable of providing a detectable signal.

CLAIM 412. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a container carrying a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable portion, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion, and one or more signal generating portions, each such portion being capable of providing a detectable signal.

CLAIM 413. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a container carrying more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a container carrying more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion to form a polynucleotide hybrid, and one or more signal generating portions, capable of providing a detectable signal.

CLAIM 414. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon comprising as components thereof:

Enz-11(C2)(D1)(C2)

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 415. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a complex which comprises:

(i) more than one molecular bridging entity, each such, entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

(ii) more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal.

CLAIM 416. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second

portion, and one or more polynucleotides which have been chemically modified or artificially altered.

CLAIM 417. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion to form a polynucleotide hybrid, and one or more polynucleotides which have been chemically modified or artificially altered.

CLAIM 418. (Previously Presented) The kit according to any of claim 411, 412, 413, 414 or 415, further comprising means to detect a signal from said signal generating portion.

CLAIM 419. (Previously Presented) The kit according to claims 416 or 417, further comprising means to detect a signal from said one or more chemically modified or artificially altered polynucleotides.

CLAIM 420. (Previously Presented) The kit according to any of claims 411, 412, 413, 414 or 415, wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is greater than 5.

CLAIM 421. (Previously Presented) The kit according to claim 420, wherein the ratio is greater than 10.

Enz-11(C2)(D1)(C2)

CLAIM 422. (Previously Presented) The kit according to any of claims 411, 412, 413, 414 or 415, wherein the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is greater than 1.

CLAIM 423. (Previously Presented) The kit according to claims 416 or 417, wherein the ratio of the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is greater than 1.

CLAIM 424. (Previously Presented) The kit according to claim 423, wherein the ratio is greater than 5.

CLAIM 425. (Previously Presented) The kit according to claim 424, wherein the ratio is greater than 10.

CLAIM 426. (Previously Presented) The kit according to, any of claims 411, 412, 413, 414 or 415, wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is greater than 1, and the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is greater than 1.

CLAIM 427. (Previously Presented) The kit according to claims 416 or 417, wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is greater than 1, and the ratio of the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is greater than 1.

CLAIM 428. (Previously Presented) The kit according to claim 426, wherein one or both ratios are greater than 5.

CLAIM 429. (Previously Presented) The kit according to claim 428, wherein one or both ratios are greater than 10.

CLAIM 430. (Previously Presented) The kit according to claim 427, wherein one or both ratios are greater than 5.

CLAIM 431. (Previously Presented) The kit according to claim 430, wherein one or both ratios are greater than 10.

CLAIM 432. (Previously Presented) The kit according to any of claims 411, 412, 413, 414, 415, 416 or 417, wherein the ratio of signalling entities to the molecular bridging entity is greater than 5.

CLAIM 433. (Previously Presented) The kit according to claim 432, wherein the ratio is greater than 10.

CLAIM 434. (Previously Presented) The kit according to any of claims 411, 412, 413, 414 or 415, wherein said signal generating portion is carried in a separate container from the container carrying the signalling entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion.

CLAIM 435. (Previously Presented) The kit according to claims 416 or 417, wherein said one or more chemically modified or artificially altered polynucleotides are carried in a separate container from the container carrying the signalling entity comprising a nucleic acid, portion capable of binding to or hybridizing with said bridging entity nucleic acid second portion.

CLAIM 436. (Previously Presented) The kit according to any of claims 411, 412, 413, 414, 415, 416 or 417, wherein said analyte comprises a biological system.

Enz-11(C2)(D1)(C2)

CLAIM 437. (Previously Presented) The kit according to any of claims 411, 412, 413, 414, 415, 416 or 417, further comprising one or more solid supports.

CLAIM 438. (Previously Presented) The composition according to claims 291, 292, 293 or 294, wherein said one or more chemically modified or artificially altered polynucleotides comprise one or more nucleic acid analogs.

CLAIM 439. (Previously Presented) The process according to claims 442, 443, 445, 447, 449, 451, 453, 455, 457, 458 or 459, wherein said step of detecting the analyte by a signal provided by said signal generating portion or portions present in said complex comprises carrying out a binding step on an insoluble phase.

CLAIM 440. (Canceled)

CLAIM 441. (Previously Presented) The composition according to claim 309, wherein the nucleic acid in said molecular bridging entity recognizing first portion and said molecular bridging entity nucleic acid second portion are incapable of hybridizing to identical oligo- or polynucleotide sequences.

CLAIM 442. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing the composition of claim 462;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 443. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

Enz-11(C2)(D1)(C2)

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 444. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 445. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

a first part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal; and

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating, portion or portions present in said complex.

CLAIM 446. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises:

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 447. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 448. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 449. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion or portions on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 450. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second

portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 451. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 452. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 453. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 454. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising;

providing a composition of matter comprising a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entitles substantially, incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising the components of said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 455. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition which comprises:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with

said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

fixing or immobilizing said analyte or a sample containing said analyte to a solid support;

forming a complex comprising, said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 456. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition of matter comprising a complex which comprises: a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portion capable of providing a detectable signal;

fixing or immobilizing said analyte or a sample containing said analyte to a solid support;

forming a complex comprising said composition and said analyte; and detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 457. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition comprising:

a first part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with

a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

fixing or immobilizing said analyte or a sample containing said analyte to a solid support;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

CLAIM 458. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

providing a composition comprising:

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

fixing or immobilizing said analyte or a sample containing said analyte to a solid support;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by said signal generating portion or portions present in said complex.

Enz-11(C2)(D1)(C2)

CLAIM 459. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

fixing or immobilizing said analyte or a sample containing said analyte to a solid support;

providing a composition comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by means of said signal generating portion or portions present in said complex.

CLAIM 460. (Previously Presented) A process for detecting an analyte having one or more molecularly recognizable portions thereon, comprising:

fixing or Immobilizing said analyte or a sample containing said analyte to a solid support;

providing a composition comprising a complex which comprises:
a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second

portion, and one or more chemically modified or artificially altered polynucleotides capable of providing a detectable signal;

forming a complex comprising said composition and said analyte; and

detecting said analyte by a signal provided by means of said signal generating portion or portions present in said complex.

CLAIM 461. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said signal generating portion or said one or more chemically modified or artificially altered polynucleotides are capable of being detected by a binding member in an insoluble phase.

CLAIM 462. (Previously Presented) The composition according to any of claims 283, 284, 286, 287, 288, 289, 291, 292, 293 or 294, wherein the nucleic acid in said molecular bridging entity recognizing first portion and said molecular bridging entity nucleic acid second portion are incapable of hybridizing to identical oligo- or polynucleotide sequences.

CLAIM 463. (Previously Presented) The composition according to any of claims 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293 or 294, wherein said molecular bridging entity comprises a polymer selected from the group consisting of a nucleic acid-protein polymer, a nucleic acid-polypeptide polymer, a nucleic acid-polysaccharide polymer and a polypeptide-polysaccharide polymer, said polymer comprising one or more chemically modified purines, one or more chemically modified pyrimidines, one or more chemically modified sugar moieties, or one or more chemically modified phosphate moieties, or a combination of any of the foregoing.

CLAIM 464. (Previously Presented) A composition of matter comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a

biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 465. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an

enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion or portions on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 466. (Previously Presented) A composition of matter comprising:
a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such

entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 467. (Previously Presented) A composition of matter comprising:
a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound,

a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 468. (Previously Presented) A composition of matter comprising:

a first part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

Enz-11(C2)(D1)(C2)

CLAIM 469. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon;

a second part which comprises more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of d virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminiescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 470. (Previously Presented) A composition of matter comprising:
a complex which comprises:

Enz-11(C2)(D1)(C2)

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 471. (Previously Presented) A composition of matter comprising:
a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;
more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable analyte portion, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a

cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said more than one bridging entity nucleic acid second portion, and one or more signal generating portions capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 472. (Previously Presented) A composition of matter comprising:

a first part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a second part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 473. (Previously Presented) A composition of matter comprising:
a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of directly or indirectly providing a detectable signal, said direct

signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 474. (Previously Presented) A composition of matter comprising:

a first part which comprises an analyte having one or more molecularly recognizable portions thereon, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof;

a second part which comprises a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

a third part which comprises one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating

portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 475. (Previously Presented) A composition of matter comprising:
a complex which comprises:

an analyte having one or more molecularly recognizable portions thereon;
a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, said analyte molecularly recognizable portion comprising a biological system selected from the group consisting of a virus or a viral component thereof and a cell or a cellular component thereof, said cell or cellular component thereof comprising a bacterium or a bacterial component thereof, said first portion being selected from the group consisting of an antigen, a polyclonal or a monoclonal antibody, a hormone, a receptor, an enzyme, an allosteric effector, an enzyme substrate, an enzyme cofactor, a protein and a protein receptor, and a second portion comprising one or more nucleic acid sequences or segments; and

one or more non-radioactive signalling entities substantially incapable of binding to or hybridizing with the molecularly recognizable portion on said analyte, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more chemically modified or artificially altered polynucleotides capable of directly or indirectly providing a detectable signal, said direct signal providing signal generating portion being selected from the group consisting of a fluorogenic compound, a phosphorescent compound, a chromogenic compound, a chemiluminescent compound, an electron dense compound, an enzyme, and said indirect signal providing signal generating portion being selected from the group consisting of an antibody, an antigen, a hapten, a receptor, a ligand, an enzyme, a polynucleotide sequence capable of recognizing a signal-containing moiety, and a compound capable of binding to an insoluble phase.

CLAIM 476. (Previously Presented) The composition according to any of claims 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474 or 475, wherein said nucleic acid sequences or segments in the molecular bridging entity second portion, or said signalling entity nucleic acid portion, or both, are derived from the group consisting of a T even phage, a filamentous phage, and a M13 phage or an M13 phage variant.

CLAIM 477. (Previously Presented) The composition according to any of claims 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474 or 475, wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from the group consisting of a number greater than 5 and a number greater than 10, and wherein the ratio of the signal generating portions or the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is selected from the group consisting of a number greater than 5 and a number greater than 10.

CLAIM 478. (Previously Presented) The composition according to claim 477, wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity, and the ratio of the signal generating portions or the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is selected from the group consisting of a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 479. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

(i) a container carrying a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable portion on said analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a container carrying more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion nucleic acid sequence or segment, and one or more signal generating portions, each such portion being capable of providing a detectable signal;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 480. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a container carrying a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable portion, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion, and one or more signal generating portions, each such portion being capable of providing a detectable signal;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is

selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 481. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a container carrying more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

a container carrying more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion to form a polynucleotide hybrid, and one or more signal generating portions capable of providing a detectable signal;
wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 482. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the signal generating portions to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 483. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a complex which comprises:

(i) more than one molecular bridging entity, each such entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

(ii) more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more signal generating portions capable of providing a detectable signal;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the signal

generating portions to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 484. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion, and one or more polynucleotides which have been chemically modified or artificially altered;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein one or both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 485. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

a complex which comprises:

a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with a molecularly recognizable portion on an analyte, and a second portion comprising one or more nucleic acid sequences or segments; and

more than one non-radioactive signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion to form a polynucleotide hybrid, and one or more polynucleotides which have been chemically modified or artificially altered;

wherein the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity is selected from a number greater than 5 and a number greater than 10; or

wherein one or both the ratio of the nucleic acid sequences or segments in the second portion to the first portion of the molecular bridging entity and the ratio of the one or more chemically modified or artificially altered polynucleotides to the nucleic acid portion in any or all of the signalling entities is selected from a number greater than 1, a number greater than 5 and a number greater than 10.

CLAIM 486. (Previously Presented) The kit of any of claims 479, 480, 481, 482 or 483, wherein said signal generating portion is carried in a separate container from the container carrying the signalling entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion.

CLAIM 487. (Previously Presented) The kit of claims 484 or 485, wherein said one or more chemically modified or artificially altered polynucleotides are carried in a separate container from the container carrying the signalling entity comprising a nucleic acid portion capable of hybridizing with said bridging entity nucleic acid second portion.

CLAIM 488. (Previously Presented) A kit for use in carrying out the process of claim 443, said kit comprising as components thereof the first part and the second part of the composition provided in said process.

CLAIM 489. (Previously Presented) A kit for use in carrying out the process of claim 444, said kit comprising as components thereof said complex provided as a composition in said process.

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CLAIM 490. (Previously Presented) A kit for use in carrying out the process of claim 445, said kit comprising as components thereof said first part and said second part provided as a composition in said process.

CLAIM 491. (Previously Presented) A kit for use in carrying out the process of claim 446, said kit comprising as components thereof said complex provided as a composition in said process.

CLAIM 492. (Previously Presented) A kit for use in carrying out the process of claim 447, said kit comprising as components thereof said first part and said second part provided as a composition in said process.

CLAIM 493. (Previously Presented) A kit for use in carrying out the process of claim 448, said kit comprising as components thereof said complex provided as a composition in said process.

CLAIM 494. (Previously Presented) A kit for use in carrying out the process of claim 449, said kit comprising as components thereof said first part, said second part and said third part provided as a composition in said process.

CLAIM 495. (Previously Presented) A kit for use in carrying out the process of claim 450, said kit comprising as components thereof said complex provided as a composition in said process.

CLAIM 496. (Previously Presented) A kit for use in carrying out the process of claim 451, said kit comprising as components thereof said first part, said second part and said third part provided as a composition in said process.

CLAIM 497. (Previously Presented) A kit for use in carrying out the process of claim 452, said kit comprising as components thereof said complex provided as a composition in said process.

CLAIM 498. (Previously Presented) A kit for use in carrying out the process of claim 453, said kit comprising as components thereof said first part, said second part and said third part provided as a composition in said process.

CLAIM 499. (Previously Presented) A kit for use in carrying out the process of claim 454, said kit comprising as components thereof said complex provided as a composition in said process.

CLAIM 500. (Previously Presented) A kit for use in carrying out the process of claim 455, said kit comprising as components thereof said first part and said second part provided as a composition and said solid support in said process.

CLAIM 501. (Previously Presented) A kit for use in carrying out the process of claim 456, said kit comprising as components thereof said complex provided as a composition and said solid support in said process.

CLAIM 502. (Previously Presented) A kit for use in carrying out the process of claim 457, said kit comprising as components thereof said first part and said second part provided as a composition and said solid support in said process.

CLAIM 503. (Previously Presented) A kit for use in carrying out the process of claim 458, said kit comprising as components thereof said composition provided and said solid support in said process.

CLAIM 504. (Previously Presented) A kit for use in carrying out the process of claim 459, said kit comprising as components thereof said first part and said second part provided as a composition and said solid support in said process.

CLAIM 505. (Previously Presented) A kit for use in carrying out the process of claim 460, said kit comprising as components thereof said complex provided as a composition and said solid support in said process.

CLAIM 506. (Canceled)

CLAIM 507. (Previously Presented) A polynucleotide sequence covalently attached to a monoclonal antibody.

CLAIM 508. (Previously Presented) A polynucleotide sequence covalently attached to a lectin.

CLAIM 509. (Canceled)

CLAIM 510. (Previously Presented) A polynucleotide sequence covalently attached to a hormone receptor.

CLAIM 511. (Previously Presented) A polynucleotide sequence covalently attached to a hormone.

CLAIM 512-527. (Canceled)

CLAIM 528. (Previously Presented) A circular DNA molecule covalently attached to a non-radiolabeled signal generating moiety that comprises an enzyme.

CLAIM 529. (Previously Presented) A circular DNA molecule comprising a polynucleotide that encodes part or all of a gene, wherein the DNA molecule is covalently attached to a non-radiolabeled signal generating moiety that comprises biotin.

CLAIM 530. (Previously Presented) A circular DNA molecule comprising a polynucleotide that encodes part or all of a gene, wherein the DNA molecule is covalently attached to a non-radiolabeled signal generating moiety that comprises an antibody.

CLAIM 531. (Previously Presented) A circular DNA molecule comprising a polynucleotide that encodes part or all of a gene, wherein the DNA molecule is covalently attached to a non-radiolabeled signal generating moiety that comprises a fluorogenic compound.

CLAIM 532. (Previously Presented) The process of claim 443, wherein said analyte is a DNA sequence, said bridging entity is a single-stranded DNA sequence, and said signalling entities are single-stranded DNA sequences.

CLAIM 533. (Previously Presented) The process of claim 532, wherein said bridging entity is derived from a filamentous phage.

CLAIM 534. (Previously Presented) The process of claim 533, wherein said signalling entities are derived from filamentous phages.

CLAIM 535. (Previously Presented) The process of claim 534, wherein said bridging entity codes for a gene product or fragment thereof, and said forming step comprises either (i) contacting said analyte with said bridging entity to form a first complex and thereafter contacting said first complex with said signalling entities to form said detectable complex or (ii) contacting said bridging entity with said signalling entities to

form a first complex and thereafter contacting said first complex with said analyte to form said detectable complex.

CLAIM 536. (Previously Presented) The process of claim 443, wherein said analyte is a polynucleotide, said one or more nucleic acid sequences or segments of said second portion are repeating low complexity nucleic acid sequences or segments, and said one or more nucleic acid sequences or segments of said second portion are incapable of hybridizing to the analyte.

CLAIM 537. (Previously Presented) The process of claim 536, wherein said signal is amplified because the ratio of the signalling entities to the bridging entity exceeds 5.

CLAIM 538. (Previously Presented) The kit of claim 411, wherein said analyte is a polynucleotide, said one or more nucleic acid sequences or segments of said second portion are repeating low complexity nucleic acid sequences or segments, and said one or more nucleic acid sequences or segments of said second portion are incapable of hybridizing to the analyte.

CLAIM 539. (Previously Presented) The kit of claim 538, wherein said signal is amplified because the ratio of the signalling entities to the bridging entity exceeds 5.

CLAIM 540. (Previously Presented) The process of claim 443, wherein said analyte is a single-stranded DNA sequence fixed to a solid support, said bridging entity comprises non-naturally occurring or artificially modified DNA, said bridging entity first portion comprises a linear single-stranded polynucleotide sequence, said bridging entity first portion is covalently bound to said bridging entity second portion, and said bridging entity second portion is single-stranded and linear and comprises more than one of said nucleic acid sequences or segments.

CLAIM 541. (Previously Presented) The process of claim 540, wherein said signalling entities are single-stranded oligo- or polynucleotide sequences, said bridging entity first portion is capable of encoding a gene product or fragment thereof, and the process further comprises one or more washing steps prior to detection.

CLAIM 542. (Previously Presented) The composition of claim 283, wherein said analyte is a single-stranded DNA sequence fixed to a solid support, said bridging entity comprises non-naturally occurring or artificially modified DNA, said bridging entity first portion comprises a linear single-stranded polynucleotide sequence, said bridging entity first portion is covalently bound to said bridging entity second portion, and said bridging entity second portion is single-stranded and linear and comprises more than one of said nucleic acid sequences or segments.

CLAIM 543. (Previously Presented) The composition of claim 542, wherein said signalling entities are single-stranded oligo- or polynucleotide sequences and said bridging entity first portion is capable of encoding a gene product or fragment thereof.

CLAIM 544. (Previously Presented) The kit of claim 411, wherein said analyte is a single-stranded DNA sequence fixed to a solid support, said bridging entity comprises non-naturally occurring or artificially modified DNA, said bridging entity first portion comprises a linear single-stranded polynucleotide sequence, said bridging entity first portion is covalently bound to said bridging entity second portion, and said bridging entity second portion is single-stranded and linear and comprises more than one of said nucleic acid sequences or segments.

CLAIM 545. (Previously Presented) The kit of claim 544, wherein said signalling entities are single-stranded oligo- or polynucleotide sequences and said bridging entity first portion is capable of encoding a gene product or fragment thereof.

CLAIM 546. (Previously Presented) A kit for the detection in a sample of an analyte having one or more molecularly recognizable portions thereon, comprising as components thereof:

(i) a container carrying a molecular bridging entity comprising a first portion capable of recognizing and binding to or hybridizing with said molecularly recognizable portion on said analyte, and a second portion comprising one, or more nucleic acid sequences or segments; and

(ii) a container carrying more than one signalling entity, each such entity comprising a nucleic acid portion capable of hybridizing with said bridging entity second portion nucleic acid sequence or segment, and one or more signal generating portions, each such portion being capable of providing a detectable signal,

wherein said analyte is a polynucleotide, said one or more nucleic acid sequences or segments of said second portion are repeating low complexity nucleic acid sequences or segments, and said one or more nucleic acid sequences or segments of said second portion are incapable of hybridizing to the analyte.

CLAIM 547. (Previously Presented) The kit of claim 546, wherein said signal is amplified because the ratio of the signalling entities to the bridging entity exceeds 5.

CLAIMS 548-552. (Canceled)

REMARKS

Status of the Claims

Claims 283-362, 364, 365, 382, 383, 400, 401, 403, 404, 406, 407, 409-439, 441-505, 507, 508, 510, 511 and 528-547 are pending. As discussed below, these claims have been allowed by the USPTO.

Statement of the Case

The above-identified application was filed on June 7, 1995. The application had 149 original claims. Claims 2-149 were canceled in the original filing papers.

On March 5, 1996, Applicants filed a preliminary amendment canceling claim 1 and adding new claims 150-282.

On April 12, 1996, Applicants filed a second preliminary amendment canceling claims 150-282 and adding claims 283-437.

On April 15, 1996, Applicants filed a supplemental to second preliminary amendment amending claims 300, 312, 330 and 412 and adding new claim 438.

On July 25, 1997, Applicants amended 56 claims and added claims 439-460.

On March 25, 1998, Applicants amended 19 claims, added new claims 461-463, and canceled claim 440.

On June 29, 1998, Applicants amended 16 claims and added new claims 464-505.

On August 25, 1999, Applicants amended 42 claims.

On January 19, 2000, Applicants added new claims 506-531.

On March 13, 2003, Applicants added new claims 532-545.

On July 23, 2003, Applicants added new claims 546 and 547.

On August 20, 2004, Applicants canceled claims 509, 512-515, and 526, amended claims 522, 516, and 524, and added claims 548 and 549.

On July 7, 2005, Applicants canceled claims 506, 516-525, 527, 548, and 549.

On September 20, 2005, Applicants added claims 550-552.

On October 21, 2005, Applicants canceled claims 366-381, 384-399, 402, 408, and 550-552.

On November 21, 2005, the USPTO allowed claims 283-362, 364, 365, 382, 383, 400, 401, 403, 404, 406, 407, 409-439, 441-505, 507, 508, 510, 511 and 528-547.

On August 7, 2006, the Board of Patent Appeals and Interferences ("Board") declared an interference between the claims of this application and U.S. Patent No. 5,124,246.

On February 22, 2010, the Board denied Patentee's threshold motions.

On February 23, 2010, the Board entered judgment for Applicants.

On May 14, 2010, the Board denied Patentee's request for reconsideration of the Board's February 22, 2010 decision.

Request for Voluntary Publication of Patent Application

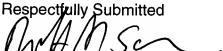
Concurrently with this paper, Applicants are filing a Request for Voluntary Publication of Patent Application. In connection with this request, Applicants respectfully request that pending and allowed claims 283-362, 364, 365, 382, 383, 400, 401, 403, 404, 406, 407, 409-439, 441-505, 507, 508, 510, 511 and 528-547 be published with the application.

SUMMARY & CONCLUSIONS

This paper is a Listing of Claims Accompanying a Request For Voluntary Publication of U.S. Patent Application Serial No. 08/479,995, filed on June 7, 1995.

Applicants have authorized the USPTO to charge its deposit account in the Request For Voluntary Publication, filed concurrently with this paper.

Respectfully Submitted



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